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| ኑ From:               | Chan, Christina                        |  |
|-----------------------|--|--|
| ₄ Sent:               | Tuesday, February 07, 2006 7:28 PM     |  |
| · To:                 | Basi, Nirmal; STIC-Biotech/ChemLib     |  |
| <sup>™</sup> Subject: | RE: Rush search for App. #: 10/083,168 |  |
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| Please musik Thanks Chris                                     |  |      | <u>.</u>        | ום.<br>רו   |                                   |
|---|--|------|-----------------|-------------|-----------------------------------|
| Chris Chan  |  |      | VCHEP<br>(STIC) | C)<br> <br> |                                   |
| TC 1600 New Hire Training (<br>(571)-272-0841<br>Remsen, 3E89 | Coordinator and SPE 1644                 |      | I. DIVICI       | 2000        | ֥.                                |
| Kenisen, 51209  | 14.11.11.14.14.14.14.14.14.14.14.14.14.1 | <br> | <u> </u>        |             | e a e e e en Pousantes acassanane |

-----Original Message-----From: Basi, Nirmal

Sent:

Tuesday, February 07, 2006 7:27 PM

To:

Chan, Christina

Subject: Rush search for App. #: 10/083,168

Thurman I am seeking approval for a RUSH sequence search for an amended case, as

indicated below. If approved, could you

please forward the search to STIC and cc a copy to me.

Examiner: Nirmal S. Basi

Art Unit 1646

Office: Remsen Building, Room 4D68 Mail Room: Remsen Building, room 4C70

Sequence search:

App. #: 10/083,168. Result format: Paper.

### Title: ENDOGENOUS AND NON-ENDOGENOUS VERSIONS OF HUMAN G PROTEIN-COUPLED RECEPTORS

Inventors:Liaw et al

Priority Date: 4/14/97 Please search:

i) SEQ ID NOs:16, 84 and 85

| ******                   | *********            | **********                        |
|--------------------------|----------------------|-----------------------------------|
| Searcher:                | Type of Search       | Vendors and cost where applicable |
| Searcher Phone:          | NA# AA#:             | STN:                              |
| Date Searcher Picked up: | S/L:Oligomer:        | DIALOG:                           |
| Date completed: 2-13-06  | Encode/Transl:       | QUESTEL/ORBIT:                    |
| Searcher Prep Time:      | Structure #: Text:   | LEXIS/NEXIS:_                     |
| Online Time:             | Inventor:Litigation: | SEQUENCE SYSTEM:                  |
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|                          |                      | Other (Specify):                  |

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Search issued, commercial and interference databases.

Thanks, Nirmal S. Basi

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GenCore version 5.1.7 (c) 1993 - 2006 Biocceleration Ltd. Copyright

OM protein - protein search, using sw model

February 9, 2006, 00:47:19 Run on:

; Search time 214.5 Seconds (without alignments) 632.951 Million cell updates/sec

US-10-083-168-16 1614 1 MNGTYNTCGSSDLTWPPAIK......AVAPRAKAHKSQDSLCVTLA 309 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2443163 Beqs, 439378781 residues Searched:

2443163 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A\_Geneseq\_21:\*
1: geneseqp1980s:\*
2: geneseqp2000s:\*
3: geneseqp2000s:\*
5: geneseqp2001s:\*
6: geneseqp2001s:\*
7: geneseqp2003as:\*
7: geneseqp2003as:\*
8: geneseqp20048:\*
9: geneseqp20048:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| SS        | Description                   | Human    | Abg95159 Human GPC | Abp82002 Human G p | Human    | Human    | Ado78094 Human GPR | Human    | Human    | Abg95172 Human GPC | _        | Orphar   | Human    | Human    | Human    | Ado78095 Human GPR | Adr10454 Human pro | Human    | Ado29395 Mouse GPC | Human    | Human    | Abg73513 Human p2y | App81870 Human G p | Human    | Adf91778 Human P2Y |
|-----------|-------------------------------|----------|--------------------|--------------------|----------|----------|--------------------|----------|----------|--------------------|----------|----------|----------|----------|----------|--------------------|--------------------|----------|--------------------|----------|----------|--------------------|--------------------|----------|--------------------|
| SUMMARIES | QI                            | AAY79576 | ABG95159           | ABP82002           | ADB67656 | AD029394 | AD078094           | ADV73203 | AEB15039 | ABG95172           | AAY69989 | ADF70461 | ADF50511 | AAY58645 | ADA84069 | AD078095           | ADR10454           | ADP29765 | AD029395           | AAW62597 | ABP61511 | ABG73513           | ABP81870           | ADH69286 | ADF91778           |
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|           | Query<br>Match                | 100.0    | 100.0              | 100.0              | 100.0    | 100.0    | 100.0              | 100.0    | 100.0    | 99.7               | 9.66     | 9.66     | 99.5     | 99.3     | 99.3     | 99.3               | 99.3               | 85.6     | 9.69               | 24.9     | 24.9     | 24.9               | 24.9               | 24.9     | 24.9               |
|           | Score                         | 1614     | 1614               | 1614               | 1614     | 1614     | 1614               | 1614     | 1614     | 1609               | 1608     | 1608     | 1606     | 1602     | 1602     | 1602               | 1602               | 1382     | 1124               | 402      | 402      | 402                | 402                | 402      | 402                |
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| Ado29049 Human nov | Human      | Human      | Human      | Human      | Adf70491 Orphan re | Human      | Adf91777 Human P2Y | Ado29050 Mouse nov | _          | Human      | Mouse      | Adw44804 Human RUP | Adw44778 Human EFA | Aeb20962 Human RUP | Human      | Adw44802 Human RUP | Adw44810 Human RUP | Adw44805 Human RUP | Adw44814 Human RUP | Aau77993 Human inf |
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| 3 ADO29049         | 3 ADQ88244 | 3 ADQ81575 | 3 ADS84260 | 9 ADV35123 | 7 ADF70491         | 7 ADH69285 | 3 ADF91777         | 3 ADO29050         | 5 ABP61510 | 3 ADS84259 | 3 ADO29415 | 9 ADW44804         | 9 ADW44778         | 9 AEB20962         | 9 ADW44807 | 9 ADW44802         | 9 ADW44810         | 9 ADW44805         | 9 ADW44814         | 5 AAU77993         |
| 370                | 370        | 370        | 370        | 370        | 809                | 370        | 370                | 370                | 370        | 368        | 327        | 363                | 363                | 363                | 363        | 363                | 363                | 363                | 363                | 363                |
| 24.9               | 24.9       | 24.9       | 24.9       | 24.9       | 24.9               | 24.8       | 24.8               | 24.6               | 24.3       | 24.2       | 23.9       | 23.6               | 23.6               | 23.6               | 23.5       | 23.5               | 23.4               | 23.4               | 23.4               | 23.3               |
| 402                | 402        | 402        | 402        | 402        | 402                | 401        | 401                | 397                | 392        | 390        | 385        | 381.5              | 381.5              | 381.5              | 379.5      | 378.5              | 377.5              | 377.5              | 377.5              | 376.5              |
| 25                 | 26         | 27         | 28         | 29         | 30                 | 31         | 35                 | 9 6                | (A)        | 35         | 96         | 37                 | 8                  | 6                  | 40         | 4                  | 4 2                | 4 ,                | 44                 | 45                 |

## ALIGNMENTS

GPR35; G protein coupled receptor; human; NIDDM1; non-insulin-dependent diabetes mellitus; CAPN10 gene; calpain 10; diagnosis; therapy. Human G protein coupled receptor GPR35 AAY79576 standard; protein; 309 AA. (first entry) 15-AUG-2000 AAY79576; RESULT 1 AAY79576 ID AAY7 

'note= "encoded by GCG" Location/Qualifiers Key Misc-difference 174 Misc-difference Homo sapiens.

/note= "encoded by AGT"

98US-0105052P. 99US-0134175P. 99WO-US024890. WO200023603-A2 21-OCT-1999; 21-OCT-1998; 13-MAY-1999; 27-APR-2000.

(ARCH-) ARCH DEV CORP. (TEXA ) UNIV OF TEXAS SYSTEM.

Otani K; Zhou Y, N, Sreenan S, S, Horikawa Y, Oda Bell GI, Cox NJ; Polonsky KS, Hanis CL, B

WPI; 2000-339702/29. N-PSDB; AAA27485, AAY79574, AAY79576.

Method for screening for type 2 diabetes mellitus comprises detecting polymorphism in a calpain encoding nucleic acid segment or a protease-encoding nucleic acid segment.

Claim 75; Page 237-238; 257pp; English.

The present sequence is that of the human gene encoding G protein coupled

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receptor, GPR35 as deduced from a composite CDNA (see AAA27485). The sequence of GPR35 is similar to that of a putative purinoceptor PPY9 (aq.11 identity) suggesting that ATP or other nucleotide is its ligand. GPR35 mRNA was detected in all adult and foetal tissues examined with relatively higher levels in adult lung, small intestine, colon and atomach. In these tissues, there are Z major transcripts of 2.4 and 4.4 kb, whareas in skeletal muscle there is a single transcript of 2.4 and 4.4 kb, whareas in skeletal muscle there is a single transcript of 2.4 and 4.4 kb, whareas in skeletal muscle there is a single transcript of 2.4 and 4.4 kb, which encodes a novel calpain-like cysteine protease, designated calpain 10. Mutations in the CARNIO gene are responsible for susceptibility to type 2 diabetes calpain-like cysteine protease, designated propensity for type 2 diabetes mellitus are based on detection of a propensity for type 2 diabetes mellitus are based on detection of a polymorphism in a calpain encoding nucleic acid. Methods are also claimed for identifying modulators of calpain activity, and using these modulators to treat diabetes, in particular through the regulation of an insulin secretory response or insulin mediated glucose transport
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# Sequence 309 AA;

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                                                                                                                                                            PLRARGLRSPRQAAAVCAVLWVLVIGSLVARWLLGIQEGGFCFRSTRHNFNSMRFPLLGF 180
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100.0%; Score 1614; DB 3; 100.0%; Pred. No. 3.1e-167;
                           0; Mismatches
                          Matches 309; Conservative
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#### ABG95159 standard; protein; 309 AA. (first entry) Human GPCR GPR35. 04-DEC-2002 ABG95159 RESULT

Human; transmembrane receptor; G-protein coupled receptor; GPCR; allergy; hypertension; reflux disease; depression; migraine; schizophrenia; ulcer; psychotic disorder; asthma; bronchospasm; anaesthesia; myocardial infarction; MI; stroke; glaucoma; anxiety; prostatic hyperplasia; epilepsy; prostate cancer; rhinitis; angina; prostatic hypertrophy; receptor.

Homo sapiens

WO200268600-A2

G protein-coupled receptor; GPCR; antigenic peptide; gene therapy; of protein-coupled receptor modulator; antibody; immune-related disease; growth-related disease; cell regeneration-related disease; immunological-related cell proliferative disease; autoimmune disease;

Human G protein-coupled receptor GPR35 protein SEQ ID NO:492.

26-FEB-2002; 2002WO-US005625.

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or inverse agonist compounds for treating diseases associated with GPCR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 PLRARGLRSPRQAAAVCAVLWVLVIGSLVARWLLGIQEGGFCRRSTRHNFNSMRFPLLGF 180
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                                                                                                                                                                                                                                                                                                                                                                 reflux disease, depression, migraîne, schizophrenia, ulcers, psychotic disorders, asthma, bronchospasm, ansesthesia, myocardial infarction (MI), stroke, glaucoma, prostatic hyperplasia, epilepsy, prostate cancer, anxiety, prostatic hypertrophy, rhinitis, and angina. The present sequence represents an endogenous human GPCR
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                                                                                                                                                                                                                                                              The present invention relates to transmembrane receptors, particularly endogenous human G-protein coupled receptors (GPCRs), mutant (nonendogenous) versions of the GPCRs, and the polynucleotide sequences encoding them. The GPCRs are settled to screening agonist or inverse agonist compounds for treating diseases associated with GPCR. Diseases that can be treated with such compounds include allergies, hypertension,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MNGTYNTCGSSDLTWPPAIKLGFYAYLGVLLVIGLLLNSLALWVFCCRMQQWTETRIYMT
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                                                                                 Leonard JN;
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100.0%; Pred. No. 3.1e-167;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                 Claim 29; Page 128-130; 201pp; English.
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                                                                               Behan DP,
             26-FEB-2001; 2001US-0271913P.
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                                              (AREN-) ARENA PHARM INC
                                                                               Chalmers DT,
Ortuno D;
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                                                                                                                              2002-706980/76.
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N-PSDB; ABS73345
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New isolated antigenic peptides e.g., for G protein-coupled receptors (GPCR), useful for diagnosing and designing drugs for treating conditions in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or
Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy; osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes; graft versus host disease; Parkinson's disease; multiple sclerosis; pain; psoriasis, anxiety; depression; schizophrenia; dementia; memory loss; mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea; hypertension; hypotension; renal disorder; rheumatoid arthritis; tramma;
                                                                                                                                                                                                                                                                                                                                             Disclosure; Fig 1; 523pp; English.
                                                                                                                                                                                                         (LIFE-) LIFESPAN BIOSCIENCES INC.
                                                                                                                                                                                                                                Brown JP;
                                                                                                                                                                                    19-DEC-2000; 2000US-0257144P.
                                                                                                                                                             19-DEC-2001; 2001WO-US050107.
                                                                                                                                                                                                                                Burmer GC, Roush CL,
                                                                                                                                                                                                                                                     WPI; 2003-046718/04.
N-PSDB; ABZ42852.
                                                                                                                                                                                                                                                                                                                         autoimmune diseases.
                                                                                                                 WO200261087-A2
                                                                                             Homo sapiens.
                                                                                                                                        08-AUG-2002
                                                                       ulcer.
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The present invention describes antigenic peptides (I) comprising: (a) any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino catids. Also described: (1) an assay for the detection of a particular G protein-coupled receptor (GPCR) or a candidate polypeptide in a sample; and (2) an isolated antibody having high specificity and high affinity or avidity for a particular GPCR. (I) can be used as GPCR modulators and in gene therapy. The antigenic peptides for GPCRs are useful in detecting an antibody against a particular GPCR. and in the production of specific antibodies. The peptides and antibodies are also useful for detecting the presence or absence of corresponding GPCRs. The antigenic peptides for GPCRs and antibodies are useful for diagnosing and designing drugs for treating immune-related diseases, immunological-related cell proliferative GPCRs and antibodies are useful for diagnosing and designing drugs for treating immune diseases, jimmunological-related cell proliferative diseases, or autoimmune diseases, immunological-related cell proliferative diseases, or autoimmune diseases, e.g. AlDS, Alzheimer's disease, concertratis, osteopromisis, cancer, cardiomyopathy, chronic and acute inflammation, allergies, Crohn's disease, graft versus host disease, Parkinson's disease, multiple sclerosis, pain, psoriasis, concertratis, dementia, member retardation, memory constraints, traum, tubers, or hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or any other disorder in which GPCRs are involved. The antibodies may be used in immunoassays and immunodiagnosis. ABZ4553 to ABZ42869 encode GPCR proteins given in ABP81019.

Cycomplification of the present invention
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Matches 309; Conservative
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121 PLRARGLRSPRQAAAVCAVLWVLVIGSLVARWLLGIQEGGFCFRSTRHNFNSMRFPLLGF 180

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      240
                                                                                 LAVGWNACALLETIRRALYITSKLSDANCCLDAICYYYMAKEFQEASALAVAPRAKAHKS 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Predicting pathological conditions in heart failure using marker genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MNGTYNTCGSSDLTWPPAIKLGFYAYLGVLLVLGLLLNSLALWVFCCRMQQWTBTRIYMT
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YLPLAVVVFCSLKVVTALAQRPPTDVGQAEATRKAARMVWANLLVFVVCFLPLHVGLTVR
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                                                                                                                                                                                                                                                                                           SEQ ID 25.
                                                                                                                                                                                                                                                                                                                Cardiant, Gene therapy; heart failure; human; G protein-coupled receptor 35; receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 111-113; 137pp; Japanese.
                                                                                                                                                                                                                                                                                           Human G protein-coupled receptor 35,
                                                                                                                                                                                                                      ADB67656 standard; protein; 309 AA.
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15-APR-2002; 2002JP-00112228.
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                                                                                                                                                                                                                                                                    (first entry)
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Matches 309; Conservative
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                                                                                                                                                    ODSLCVTLA 309
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2003-679959/64.
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Transgenic mouse; neurological disorder; adrenal gland disorder;

Transgenic mouse; neurological disorder; adrenal gland disorder;

Colon disorder; intestinal disorder; adrenal gland disorder;

Colon disorder; blood disorder; immune disorder; bone disorder;

Joint disorder; metabolic disorder; nutritive disorder; cancer;

Widney disorder; metabolic disorder; nutritive disorder; cancer;

Widney disorder; metabolic disorder; prostate disorder; testis disorder;

Widney disorder; thyroid disorder; pancreas disorder; spleen disorder;

Whuse disorder; thyroid disorder; matiparkinsonian; antimanic;

Wytoeratic; antiinflammatory; vasotropic; antidanginal; antiarrhythmic;

Wytoeratic hepatotropic; antibarchinsomian; antidabetic;

Wirucide; hepatotropic; antibarchinial; antidaleric; antisacterial; antidaleric; antidabetic;

Wytomacological; antiulcer; antithyroid; antidalergic; anorectic;

Mimmunosuppressive; hepatotropic; gene therapy; GPCR modulator; human;
                                                  YLPLAVVVFCSLKVVTALAQRPPTDVGQAEATRKAARMVWANLLVFVVCFLPLHVGLTVR 240
                                                                                                                                            The invention relates to human and mouse G protein-coupled receptors (GPCRs) and nucleic acids encoding them. The invention also relates to sequences at least 90% identical to the GPCR proteins and nucleic acids of the invention; methods of treating, preventing or diagnosing diseases
YLPLAVVVFCSLKVVTALAQRPPTDVGQAEATRKAARMVWANLLVFVVCFLPLHVGLTVR
                                                                                                                      LAVGWNACALLETIRRALYITSKLSDANCCLDAICYYYMAKEFQEASALAVAPRAKAHKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel mammalian G protein coupled receptors, useful for identifying compounds that modulates diagnosing and treating disease condition associated with GPCR dysfunction e.g. autoimmune diseases, angina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Li F;
Zeng H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3A, Bergmann JE, Gragerov A, Hohmann J,
Mcilwain KL, Pavlova MN, Vassilatis D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 151; SEQ ID NO 496; 542pp; English.
                                                                                                                                                                                                                                                                                                                         ADO29394 standard; protein; 309 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Human GPCR GPR35, SEQ ID NO:496.
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                                                                                                                                                                                                                                                                                                                                                                                            29-JUL-2004 (first entry)
                                                                                                                                                                                               309
                                                                                                                                                                                                                                  ODSLCVTLA 309
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compounds useful in the treatment of GPCR-related diseases; a transgenic compounds useful in the treatment of GPCR-related diseases; a transgenic mouse comprising a GPCR gene of the invention; a mouse comprising a comprising a GPCR gene of the invention; a mouse comprising derived from the transgene or in an endogenous GPCR gene; cells derived from the transgenic mice; kits comprising several mice, each of which has a mutation in a different GPCR gene of the invention, and kits comprising comprising a GPCR moteled of the invention. The invention further discloses variants of the GPCR polypeptides and vectors comprising a GPCR nucleic acids and proceed any of diseases including neurological disorders (e.g., Alzheimer's disease, diseases or schizophrenia); cells acids and proceed any comprisions of the adrenal gland; disorders (e.g., Alzheimer's disease, distributions or intestine cells. Cohn's disease, diarrhoea, food poisoning or irritable bowel cells. Crohn's disease, diarrhoea, food poisoning or irritable bowel cells. Crohn's disease, diarrhoea, food poisoning or irritable bowel cells of the adrenal gland; disorders (e.g., autoimmune disorders (e.g., angena, cardiac arrhythmia or myocardial infarction); muscular disorders (e.g., autoimmune disorders (e.g., angena, blood disorders (e.g., anthitis, gout or osteoporosis); metabolic or nutritive disorders of the kidney, liver, lung, breast, ovary, uterus, prostate, testis, skin, stomach, pancreas, spleen, thymus and thyroid (e.g., cancers). The present sequences not shown were obtained in the celetronic format directly frow Wilpo at the printed specification; those sequences not shown were obtained in celetronic format directly frow WIND at
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ive 0; Mismatches 0;
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Best Local Similarity 100.
Matches 309; Conservative
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                                                                                                                                                                                                                                                                                      The invention relates to pharmaceutical compositions that comprise an agent that inhibits the expression or activity of a tumour-associated antigen (TAg) that is encoded by a nucleic acid. The pharmaceutical compositions and related compositions, are used for treatment of diseases associated with (abnormal) expression of TAg, specifically cancer e.g. of lung, breast, prostate, colon, stomach, pancreas, ear/nose/throat, kidney or cervix, also melanoma. Compositions containing TAg, or related nucleic acid, antibodies or host cells, are also useful for diagnosis and sequence of a human GPR35.
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                                                                                                                                                                                                                Composition containing inhibitor of expression or activity of specific tumor-associated antigens, useful for treating cancers, also related compositions for diagnosis and monitoring.
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100.0%; Score 1614; DB 8; Length 309;
Best Local Similarity 100.0%; Pred. No. 3.1e-167;
Matches 309; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                     Claim 72; SEQ ID NO 9; 124pp; German.
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                                                                                                                                                          Koslowski
                                                                                    22-NOV-2002; 2002DE-01054601
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QDSLCVTLA 309
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N-PSDB; ADO78086.
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               sapiens
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New antibody that immunospecifically binds to p-cadherin, useful in preparing a composition for treating or preventing a cancer-associated disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MNGTYNTCGSSDLTWPPAIKLGFYAYLGVLLVLGLLLNSLALWVFCCRMQQWTETRIYMT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to an antibody immunospecifically binds to p-cadherin or its fragment. The antibody is useful in preparing a composition for treating or preventing a cancer-associated disorder. present sequence represents the amno acid sequence of a protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 309;
                                                                                                                                                                                                                                                                                                           Klein BK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 1614; DB 9;
100.0%; Pred. No. 3.1e-167;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                        Bu JJ, Head RD, Hippenmeyer PJ, A, Staten NR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; SEQ ID NO 44; 257pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    upregulated in human colon cancer cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein; 309 AA.
cancer; neoplasm; cytostatic
                                                                                                                                                                             28-OCT-2003; 2003WO-US034019
                                                                                                                                                                                                                       29-OCT-2002; 2002US-0422176P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            08-SEP-2005 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 309; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ODSLCVTLA 309
                                                                                                                                                                                                                                                                 (PHAA ) PHARMACIA CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ODSLCVTLA 309
                                                                                                                                                                                                                                                                                                                                                                            WPI; 2005-039958/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; ADV73165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 309 AA;
                                                                                     WO2004110345-A2
                                                                                                                                                                                                                                                                                                                                  Mazzarella RA,
                                            Homo sapiens
                                                                                                                                 23-DEC-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AEB15039;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121
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protein; 309

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ADV73203

ADV73203 ID ADV7 XX ADV7 AC ADV7 XX IO-M

10-MAR-2005 (first entry)

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the invertion relatice to the use of numban G-protein coupled receptor 35 (GRR35) for screening therapeutic agents useful in the treatment of cardiovascular disorders, liver and gastrointestinal diseases, cancer disorders, inflammatory diseases, metabolic diseases, hematological disorders, inflammatory diseases, metabolic diseases, hematological disorders, in a mammal. GPR35 is a G-protein coupled receptor (GPCR). The cast compound to the cast compound to the cast compound to the cast specified diseases in a mammal comprising determining the above specified diseases in a mammal comprising determining the amount of the GPR35 polymelectide in a sample taken from the mammal, and determining the amount of the GPR35 polymelectide in healthy and/or diseased mammals of GPR35 polymelectide in healthy and/or diseased mammals. (CRR35 polymelectide in healthy and/or diseased mammals.) (CRR35 polymelectide in healthy specified diseases in the mammal.) (CRR35 polymelectide) (3) use of regulators of a GPR35 for the preparation of the pharmaceutical composition or for the regulation of GPR35 activity in a mammal having the above specified diseases; and (4) a method for the preparation of the pharmaceutical composition or for the regulator ameliorates the symptoms of the above specified diseases; and mammal, and combining the captabator with an acceptable pharmaceutical capants for treating cardiovascular disorders, inflammatory diseases, and gastrointestinal diseases, cancer disorders, inflammatory diseases, neurological disorders and urological disorders, respiratory diseases, concerdisorders in a mammal, e.g. humans (preferably), dogs, cats, cows, horses, rabbits, and monkeys. This
                                                                                          screening; cardiovascular disease; gastrointestinal disease;
liver disease; cancer; neoplasm; metabolic disorder;
hematological disease; respiratory disease; inflammation;
neurological disease; urological disorder; cardiovascular-gen.;
gastrointestinal-gen.; hepatotropic; cytostatic; metabolic; antianemic;
respiratory-gen.; antiinflammatory; neuroprotective; uropathic; receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Screening of therapeutic agents useful in treating specified diseases involves contacting test compound with G-protein coupled receptor GPR35, and detect binding of test compound to polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   invention relates to the use of human G-protein coupled receptor 35
                                                                        G-protein coupled receptor 35; GPR35; G-protein coupled receptor; GPCR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Summer H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure, SEQ ID NO 2, 96pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Geerts A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12-DEC-2003; 2003EP-00028614.
                                                                                                                                                                                                                                                                                                                                                                                                                        02-DEC-2004; 2004WO-EP013679.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (FARB ) BAYER HEALTHCARE AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Brueggemeier U,
                    Human GPR35 polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2005-506223/51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AEB15038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 309 AA;
                                                                                                                                                                                                                                                                                                                        WO2005059546-A2.
                                                                                                                                                                                                                                                                             Homo sapiens
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                                                                           1 MNGTYNTCGSSDLTWPPAIKLGFYAYLGVLLVLGLLLNSLALWVFCCRMQQWTBTRIYMT
                                                                                                         MNGTYNTCGSSDLTWPPAIKLGFYAYLGVLLVLGLLLNSLALWVFCCRMQQWTETRIYMT
                                       Gaps
                                     ö
Length 309;
                                 0; Indels
                   3.1e-167;
100.0%; Score 1614; DB 9;
100.0%; Pred. No. 3.1e-167;
iive 0; Mismatches 0;
                 Local Similarity 100.
1es 309; Conservative
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Query Match

Best Loca Matches

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61 NLAVADLCLLCTLPFVLHSLRDTSDTPLCQLSQGIYLTNRYMSISLVTAIAVDRYVAVRH 120

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The present invention relates to transmembrane receptors, particularly endogenous human G-protein coupled receptors (GPCRs), mutant (nonendogenous) versions of the GPCRs, and the polynucleotide sequences encoding them. The GPCRs are useful for screening agonist or inverse agonist compounds for treating diseases associated with GPCR. Diseases reflux disease, depression, magraine, schizophrenia, ulcers, psychotic disorders, asthma, bronchospasm, anaesthesia, myocardial infarction (MI), stroke, glaucoma, prostatic hyperplasia, epilepsy, prostate cancer, anxiety, prostatic hyperplasia, epilepsy, prostate cancer, sequence represents a mutant human GPCR.
180
                                                                                                                    181 YLPLAVVVFCSLKVVTALAQRPPTDVGQARATRKAARMVWANLLVFVVCFLPLHVGLTVR 240
                                                                                                                                                       240
                                                                                                                                                                                         LAVGWNACALLETIRRALYITSKLSDANCCLDAICYYYMAKEFQEASALAVAPRAKAHKS 300
                                                                                                                                                                                                          241 LAVGWNACALLETIRRALYITSKLSDANCCLDAICYYYWAKERQEASALAVARRAKHKS 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; transmembrane receptor; G-protein coupled receptor; GPCR; allergy; hypertension; reflux disease; depression; migraine; schizophrenia; ulcer; psychotic disorder; asthma; bronchospasm; anaesthesia; myocardial infarction; MI; stroke; glaucoma; anxiety; prostatic hyperplasia; epilepsy; prostate cancer; rhinitis; angina; prostatic hypertrophy; receptor; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New human G-protein coupled receptor (GPCR), useful for screening agonist or inverse agonist compounds for treating diseases associated with GPCR.
                                                                      121 PLRARGLRSPRQAAAVCAVLWVLVIGSLVARWLLGIQEGGFCFRSTRHNFNSMRFPLLGF
                                                                                                                                           181 YLPLAVVVFCSLKVVTALAQRPPTDVGQAEATRKAARRWWANLLVFVVCFLPLHVGLTVR
                                                   121 PLRARGLRSPRQAAAVCAVLWVLVIGSLVARWLLGIQEGGFCFRSTRHNFNSMRFPLLGF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Behan DP, Maciejewski-Lenior D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 2; Page 189-190; 201pp; English.
                                                                                                                                                                                                                                                                                                                                                                              ABG95172 standard; protein; 309 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human GPCR GPR35 mutant A216K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-FEB-2002; 2002WO-US005625.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-FEB-2001; 2001US-0271913P.
                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chalmers DT,
                                                                                                                                                                                                                                                          QDSLCVTLA 309
                                                                                                                                                                                                                                                                                         301 ODSLCVTLA 309
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ortuno D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; ABS73401
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human receptor-associated protein; HRAP; Incyte clone 3083742; cytostatic; immunomodulatory; antiinflammatory; cardiant; antianaemic; antiarthritic antirhemuatic; antiataterthridic antirhemuatic; antiatathmatic; osteopathic; antiallergic; antidiabetic; dermatological; neuroprotective; diagnosis; treatment; prevention; reproductive disorder; cardiovascular; cell proliferative; autoimmune; inflammatory; allergy; gastrointestinal; atherosclerosis; cirrhomis; leukaemia; cancer; AIDS; arthitis; anaemia; aethma; dermatitis; diabetes; osteoporosis; multiple sclerosis; irritable bowel syndrome.
                                                                                                                                                                                                                                      180
                                                                                                                                                                                                                                                                                                                                    PLRARGLRSPROAAAVCAVLWVLVIGSLVARWLLGIQEGGFCFRSTRHNFNSMRFPLLGF 180
                                                                                                                                                                                                                                                                                                                                                                           YLPLAVVVPCSLKVVTALAORPPTDVGQAEATRKÁAŘHVMANLLVPVVCFLPLHVGLTVR 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NLAVADLCLLCTLPFVLHSLRDTSDTPLCQLSQGIYLTNRYMSISLVTAIAVDRYVAVRH 120
                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                               PLRARGLRSPRQAAAVCAVLWVLVIGSLVARWLLGIQEGGFCFRSTRHNFNSMRFPLLGF
                                                                                                                                                     1 MNGTYNTCGSSDLTWPPAIKLGFYAYLGVLLVLGLLLNSLALWVFCCRMQQWTETRIYMT
                                                                                     Gaps
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                                           Length 309;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human receptor-associated protein from Incyte clone 3083742.
                                                                                   1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note= "Potential phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Potential phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note= "Potential phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ./note= "Potential phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note= "Potential N-glycosylation site"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note= "Potential phosphorylation site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     label= Signature_sequence
'note= "G-protein_coupled receptor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Potential phosphorylation
                                           Score 1609; DB 5;
Pred. No. 1.1e-166;
                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY69989 standard; protein; 309 AA
                                         99.78;
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/label= Si
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                                                                                     Matches 308; Conservative
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238
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                                                                 Best Local Similarity
    Sequence 309 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Modified-site
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                                           Query Match
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AAY69989
ID AAY6989
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The present sequence is human receptor-associated protein (HRAP) from Incyte clone 3083742 obtained from OVARTUNOI cDNA library. This sequence is expressed in haemacropoletic/immune, gastrointestinal and reproductive tissues. HRAP has cytostatic, immunomodulatory, antianflammatory, cardiant, antiarteriosclerotic, hepatotropic, antiantentic, antiantentic, antiantentic, antiantentic, antiantentic, antiantentic, antiantentic, sequence antidiabetic, dematological and neuroprotective activities. The present sequence is useful in the diagnosis, treatment and prevention of disorders associated with HRAP expression, especially cell proliferative, autoimmunefinifammatory, reproductive, cardiovascular and gastrointestinal disorders (e.g. atherosclerosis, cirrhosis, leukaemia, cancer, AIDS, arthritis, allergies, anaemia, asthma, dermatitis, diabetes, osteoporosis, multiple sclerosis and irritable bowel syndrome)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 NLAVADLCLLCTLPFVLHSLRDTSDTPLCQLSQGIYLTNRYMSISLVTAIAVDRYVAVRH 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New human receptor-associated proteins (HRAP) useful for the diagnosis, treatment and prevention of cell proliferative, autoimmune, inflammatory, reproductive, cardiovascular, and gastrointestinal disorders.
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                                                                               /note= "Potential phosphorylation site"
                       /note= "Potential phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tang YT, Gorgone GA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99.6%; Score 1608; DB 3;
99.7%; Pred. No. 1.4e-166;
ive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 76; 99pp; English.
                                                                                                                                                                                                                                                        99WO-US017777.
                                                                                                                                                                                                                                                                                                             98US-0160065P.
98US-0098703P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lal P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 308; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Yue H, L
Baughn MR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-205710/18.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAZ50891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 309 AA;
                                                                                                                                          WO200008155-A2
Modified-site
                                                        Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hillman JL,
Corley NC, 1
                                                                                                                                                                                                                                                        06-AUG-1999;
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241 LAVGWNACALLETIRRALYITSKLSDANCCLDAICYYYMAKEFQEASALAVAPRAKAHKS 300
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                                                                                                                                                                                                                  ADF50511 standard; protein; 309 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-APR-2003; 2003WO-JP004840.
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                                                                                               301 ODSLCVTLA 309
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Obinata M;
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                                                   301 QDSLCVTLA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nishi T,
                                                                                                                                                                                                                                                                  ADF50511;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This invention relates to a novel method of identifying ligands to an orphan receptor protein which comprises transforming cells with DNA encoding a fusion protein of the orphan receptor with a fluorescent protein, so that the fusion protein is expressed in the cells (or cell membranes isolated from them) and contacting the cells with the potential ligand to be tested. A suitable fluorescent protein for incorporation in the fusion protein is green fluorescent protein (GFP), for example GFP-1, wild-type GFP, GFPUV or Enhanced GFP (EGFP). The method is useful for the identification of ligands binding to an orphan receptor protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 NLAVADLCLLCTLPFVLHSLRDTSDTPLCQLSQGIYLTNRYMSISLVTAIAVDRYVAVRH 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Transformation of cells with a fusion protein of an orphan receptor protein with a fluorescent protein useful for identification of ligands
                                                                                                                                                                                                                                     ligand; orphan receptor protein; fusion protein; fluorescent protein; cell expression; green fluorescent protein; GPP; GPP-1; wild-type GPP; GFPuv; Enhanced GPP; EGFP; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MNGTYNTCGSSDLTWPPAIKLGFYAYLGVLLVLGLLLNSLALWVFCCRMQOWTETRIYMT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ogi K, Komatsu H, Kawamata Y,
                                                                                                                                                                                       Orphan receptor ligand-related human protein SeqID84.
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99.64; Score 1608; DB 7;
Best Local Similarity 99.74; Pred. No. 2.8e-166;
Matches 308; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; SEQ ID NO 84; 594pp; Japanese.
                                                ADF70461 standard; protein; 547 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22-FEB-2002; 2002JP-00045728.
23-JUL-2002; 2002JP-00213949.
11-OCT-2002; 2002JP-00298237.
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                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the orphan receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pujii R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2003-697654/66
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                                                                                                                                                                                                                                                                                                                                       Homo sapiens
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                                                                                               ADP70461;
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RESULT 11

ADF70461

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This invention relates to a novel method for obtaining a DNA that encodes a peptide acting as agonist, antagonist or inverse agonist on a target creeptor. Specifically, it comprises transformation of endocrine cell innes originating from mammalian hypothalamus and pancreatic islets, culturing the transformants and contacting with cells expressing the target receptor. The identification of those cells with a response reaction can be used for selecting a transformant cell line with the appropriate target activity that is expressing the novel transformed DNA. Accordingly, the present invention describes novel cell lines that are applicable in expression cloning systems of bloactive peptide precursor genes, and in screening GPCR ligands for use as drugs including agonists, antagonists and inverse agonists i.e. activators and inhibitors. Such cell lines can provide a highly sensitive and convenient GPCR ligand assay system. This polypeptide sequence is the human GPCR GPR35 D133A mutein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Endocrine cell lines originated from mammalian hypothalamus and pancreatic islet, applicable in expression cloning systems of bioactive peptide precursor genes, and in screening G protein-coupled receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kunitomo H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MNGTYNTCGSSDLTWPPAIKLGFYAYLGVLLVLGLLINSLALWVFCCRNQQWTETRIYMT
                                                                                      mutant; mutein; transformation; endocrine cell line; expression cloning system; bioactive peptide; GPCR ligand; human.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "Wild type Asp substituted by Ala"
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Human GPCR GPR35 D113A mutein (SeqID 191).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence represents human GPR35A, a novel member of the purinergic family of polypeptides and a G-protein coupled receptor. The invention provides GPR35A polypeptides having at least 70% identity with the present sequence, GPR35A polymucleotides, recombinant materials, and methods for their production. GPR35A polypeptides can be used for identifying agonists and antagonists/inhibitors, and for detecting diseases associated with inappropriate GPR35A activity or levels. GPR35A polypeptides and polymucleotides, agonists, antagonists and antibodies are used to treat: infections such as bacterial, fungal, protozoan and viral infections, particularly HIV-1 and HIV-2; pain; cancer; diabetes;
                                                                                                                                240
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 9
                                                                                                                                                                                                                                                                                                                                                                   GPR35A; human; G-protein coupled receptor; purinergic; 7-transmembrane receptor; antibiotic; antifungal; antiviral; analgesic; cytoeteatic; antidiametic; antiparkinsonian; hypotensive; hypertensive; osteopathic; antianginal; cardiant; cerebroprotective, antiulcer; antiallergic; antimigraine; antiemetic; tranquillier; antidepressant; neuroleptic; notropic; anticonvulsant; tranquillier; antidepressant; neuroleptic; notropic; anticonvulsant;
                                 181 YLPLAVVVPCSLKVVTALAQRPPTDVGQAEATRKAARMVWANLLVPVVCFLPLHVGLTVR
MNGTYNTCGSSDLTWPPAIKLGFYAYLGVLLVLGLLLNSLALWVFCCRMQQWTETRIYMT
                     NLAVADLCLLCTLPFVLHSLRDTSDTPLCQLSQGIYLTNRYMSISLVTAIAVDRYVAVRH
                                                                PLRARGLRSPROAAAVCAVLWVLVIGSLVARWLLGIQEGGFCFRSTRHNFNSMRFPLLGF
                                                                                                           YLPLAVVVPCSLKVVTALAQRPPTDVGQAEATRKAARMVWANLLVFVVCFLPLHVGLTVR
                                                                                                                                                      LAVGWNACALLETIRRALYITSKLSDANCCLDAICYYYMAKEFQEASALAVAPRAKAHKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New human GPR35A polypeptides and polynucleotides used to identify agonists, antagonists and inhibitors for use in therapy.
                                                                                                                                                                                                                                                                                                                                                  Human G-protein coupled receptor GPR35A.
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                                                                                                                                                                                                                                                                                 AAY58645 standard; protein; 309
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                                                                                                                                                                                                                                                                                                                                                                                                                                         therapy; diagnosis; vaccine.
                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                   ODSLCVTLA 309
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ODSLCVTLA 309
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N-PSDB; AAZ35390.
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            failure; hypotension; hypertension; urinary retention; osteoporosis; angina pectoris; myocardial infarction; stroke; ulcers; allergy; benign prostatic hypertrophy; migraine; vomiting; psychotic and neurological disorders including anxiety, schizophrenia, manic depression, depression, delirium, dementia and severe mental retardation; and dyskinesias such as Huntingdon's or Gilles de la Tourette's syndrome. The polypeptide is also useful for production of vaccines
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Krukovskaya LL;
                                                                                                                                                                                                                                                                                                                       MNGTYNTCGSSDLTWPPAIKLGFYAYLGVLLVLGLLLNSLALWVFCCRMQQWTETRIYMT
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obesity; anorexia; bulimia; asthma; Parkinson's disease; acute heart
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                                                                                                                                                                                                                  Length 309;
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Pred. No. 6.3e-166;
0; Mismatches 2;
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22-OCT-2001; 2001US-0330457P.
19-FEB-2002; 2002US-0357144P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                           Best Local Similarity 99.4 Matches 307; Conservative
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N-PSDB; ADA84068.
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                                                                                                                                                                                Sequence 309 AA;
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stress-induced
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Determining if a nucleic acid is a marker for a phenotype/cell type of interest, by global comparison of expressed sequence tags known to be expressed in the phenotype/cell type with all ESTs expressed in normal
                                       Claim 29; Page 448-449; 516pp; English.
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The invention relates to a novel method for determining if a nucleic acid is a marker for a predetermined phenotype/cell type of interest from a CC is a group of expressed sequence tags (BSTS) known to be expressed in the comparison of a group of expressed sequence tags (BSTS) known to be expressed in the comparison of a group of expressed sequence tags (BSTS) known to be expressed in the comparison of in order to identify BSTS that are preferentially expressed in the phenotype/cell type of interest tare preferentially expressed in the comparison of the invention is useful for Arabidospsis or human. The cell type of interest from a biological species, preferably cas a tumour cell, and the predetermined phenotype is a stress induced phenotype such as hyperosmotic stress or high salt conditions. A method of the invention is also useful for detecraining the progression of colon cancer in a human, for detecting a tumour cell, and for regulating or preventing the growth of a tumour cell. An antibody of the invention is useful for detecting a tumour cell, and for regulating or tumour-associated markers. A polypeptide of the invention is useful as an imman. The present sequence represents a cumour-associated antigen of the invention.

# Sequence 309 AA;

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LAVGWNACALLETIRRALYITSKLSDANCCLDAICYYYMAKBPQEASALAVAPRAKAHKS 300
                                                                                                                                                                                                 PLRARGLRSPROAAAVCAVLWTVIGSLVARWLLGIOEGGFCPRSTRHNFNSWAFPLLGF 180
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                                                                                                                                                                                                                                                           YLPLAVVVFCSLKVVTALAQRPPTDVGQARATRKAARMVWANLLVFVVCFLPLHVGLTVR 240
                                                                                                                       NLAVADLCLLCTLPFVLHSLRDTSDTPLCQLSQGIYLTNRYMSISLVTAIAVDRYVAVRH 120
                                                                                                                                                                                PLRARGLRSPRQAAAVCAVLWVLVIGSLVARWLLGIQEGGPCPRSTRHNFNSMRFPLLGF 180
                                                                                                                                                61 NLAVADLCLLCTLPFVLHSLRDTSDTPLCQLSQGIYLTNRYMSISLVTAIAVDRYVAVRH 120
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                                                                             MNGTYNTCGSSDLIWPPAIKLGFYAYLGVLULLUSLLINSLALWVFCCRWQQWTETRIYMT
                                                                                                                                                                                                                                          YLPLAVVVPCSLKVVTALAQRPPTDVGQAEATRKAARMVMANLLVPVVCFLPLHVGLTVR
                                                           1 MNGTYNTCGSSDLTWPPAIKLGFYAYLGVLLVLGLLLNSLALWVFCCRMQQWTETRIYMT
                               Gaps
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Length 309;
                             2; Indels
99.3%; Score 1602; DB 6; 99.4%; Pred. No. 6.3e-166; iive 0; Mismatches 2;
            Best Local Similarity 99.4 Matches 307; Conservative
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tumour-associated antigen; TAg; cancer; lung cancer; breast cancer; prostate cancer; colon cancer; stomach cancer; pancreatic cancer; ear cancer; nose cancer; throat cancer; kidney cancer; cervical cancer; melanoma; tumour; human; GPR35.
              ADO78095 standard; protein; 394 AA
                                                                       (first entry)
                                                                                                  Human GPR35 isoform.
                                                                       26-AUG-2004
                                            ADO78095;
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The invention relates to pharmaceutical compositions that comprise an agent that inhibits the expression or activity of a tumour-associated artigen (TAg) that is encoded by a nucleic acid. The pharmaceutical compositions and related compositions, are used for treatment of diseases associated with (abnormal) expression of TAg, specifically cancer e.g. of lung, breast, prostate, colon, stomach, pancreas, ear/nose/throat, kidney or cervix, also melanoma. Compositions containing TAg, or related nucleic acid, antibodies or host cells, are also useful for diagnosis and monitoring of tumours. The present sequence represents the amino acid sequence of a human GPR35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 NLAVADLCLLCTLPFVLHSLRDTSDTPLCQLSQGIYLTNRYMSISLVTAIAVDRYVAVRH 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               expression or activity of specific or treating cancers, also related
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tumor-associated antigens, useful for tres
compositions for diagnosis and monitoring.
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                                                                                                                                                                                                                                                                                                             22-NOV-2002; 2002DB-01054601.
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Best Local Similarity
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                                                                           DE10254601-A1
       Homo sapiens
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sw model protein search, using OM protein ; Search time 26.5 Seconds (without alignments) 1121.924 Million cell updates/sec February 9, 2006, 00:55:13 Run on:

US-10-083-168-16 1614 1 MNGTYNTCGSSDLTWPPAIK......AVAPRAKAHKSQDSLCVTLA 309 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 of hits satisfying chosen parameters: Total number

283416 segs, 96216763 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 su

summaries

piri:
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piri:
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piri: Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

|    | Description    |   | a      | G protein-coupled | G protein-coupled |        | G protein-coupled | ATP receptor P2u - | G protein-coupled | G protein-coupled | bradykinin B2 rece | bradykinin recepto | platelet-activatin | P-2U nucleotide re |        | G protein-coupled | bradykinin B1 rece | platelet-activatin | G protein-coupled | P2Y receptor - bov | G protein-coupled | G protein-coupled | platelet-activatin | P2Y6 receptor - hu | angiotensin II rec | chemokine (C-C) re | G protein-coupled |        | bradykinin B2 rece | somatostatin recep | somatostatin recep |
|----|----------------|---|--------|-------------------|-------------------|--------|-------------------|--------------------|-------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------|-------------------|--------------------|--------------------|-------------------|--------------------|-------------------|-------------------|--------------------|--------------------|--------------------|--------------------|-------------------|--------|--------------------|--------------------|--------------------|
|    | ID             |   | JC5549 | I50241            | 169202            | T09508 | 155450            | A47556             | S33733            | 868679            | JQ1488             | OORTB2             | S13638             | A54946             | 153033 | A57641            | S60024             | A40191             | B57641            | JC4162             | S68207            | JC4737            | \$43252            | JC4800             | JC2543             | A43113             | B45680            | 863666 | 149519             | I57955             | JN0763             |
|    | DB             | - | 7      | ~                 | ~                 | ~      | 7                 | N                  | ~                 | 7                 | ~                  | -                  | 7                  | ~                  | 7      | ~                 | (7                 | ~                  | ~                 | ~                  | ~                 | ~                 | ~                  | ~                  | ~                  | ~                  | ~                 | ~      | ~                  | ~                  | N                  |
|    | Length         |   | 370    | 308               | 387               | 344    | 328               | 373                | 362               | 365               | 364                | 366                | 342                | 375                | 354    | 362               | 352                | 342                | 362               | 373                | 362               | 373               | 341                | 328                | 363                | 352                | 361               | 341    | 366                | 363                | 364                |
| do | Query<br>Match |   | 24.8   | 22.8              | 22.8              | 22.3   | 19.8              | 19.8               | 19.7              | 19.5              | 19.4               | 19.4               | 19.2               | 19.1               | 18.9   | 18.9              | 18.9               | 18.8               | 18.7              | 18.7               | 18.7              | 18.5              | 18.2               | 18.0               | 17.9               | 17.9               | ٠                 | 17.5   | 17.4               | 17.3               | 17.3               |
|    | Score          |   | 401    | 368.5             | 368.5             | 360.5  | 319               | 319                | 318               | 315.5             | 312.5              | 312.5.             | 310                | 308.5              | 305.5  | 305.5             | 305                | 304                | 302.5             | 302.5              | 301.5             | 298.5             | 293                | 291                | 289                | 288.5              | 285.5             | 283    | 281.5              | 279.5              | 279.5              |
|    | Result<br>No.  |   | 1      | 7                 | ٣                 | 4      | ß                 | v                  | 7                 | 60                | 6                  | 10                 | 11                 | 12                 | 13     | 14                | 15                 | 16                 | 17                | 18                 | 19                |                   | 21                 | 22                 | 23                 | 24                 | 25                | 26     | 27                 | 28                 | 29                 |

| angiotensin II rec | G protein-coupled | angiotensin II rec | somatostatin recep | macrophage inflamm | thrombin receptor | G protein-coupled | G protein-coupled | HHRF3 protein - hu | somatostatin recep | G protein-coupled | G protein-coupled | chemokine (C-C) re | somatostatin recep | somatostatin recep | somatostatin recep |
|--------------------|-------------------|--------------------|--------------------|--------------------|-------------------|-------------------|-------------------|--------------------|--------------------|-------------------|-------------------|--------------------|--------------------|--------------------|--------------------|
| A49092             | JC5653            | 148261             | I57940             | I49339             | 151667            | T09353            | 868208            | QQBED3             | A46226             | JC5067            | JC5068            | A45177             | A41795             | C41795             | A39297             |
| ~                  | ~                 | ~                  | ~                  | ~                  | ~                 | 7                 | ~                 | -                  | ~                  | 7                 | N                 | ~                  | ~                  | N                  | 7                  |
| <u>~</u>           |                   | ~                  | m                  | 'n                 | 0                 | _                 |                   |                    |                    |                   |                   |                    |                    |                    |                    |
| 36                 | 361               | 36                 | 36                 | 35                 | 42                | 32                | 365               | 323                | 418                | 355               | 369               | 355                | 391                | 391                | 391                |
|                    |                   |                    |                    |                    |                   |                   |                   |                    |                    | 16.5 355          |                   |                    |                    |                    |                    |
|                    |                   | 17.0               |                    |                    |                   |                   |                   | 16.7               |                    |                   | 16.3              |                    | 16.3               | 16.3               | 16.3               |

## ALIGNMENTS

RESULT 1

heptahelical P2Y5-like receptor - human

Gaps 42; Length 370; Query Match

24.8%; Score 401; DB 2; Length 370
Best Local Similarity 34.0%; Pred. No. 1.9e-29;
Matches 105; Conservative 58; Mismatches 104; Indels Query Match

44 AVYSVVPILGLITNSVSLEVFCFRAMGARSETAIFITNLAVSDLLFVCTLPFKIFYNFNRH 103 81 25 AYLGVLLVIGLLINSLALWVFCCRMQQWTETRIYMTNIAVADLCLLCTLPF-VLHSLR--ઠે 셤

82 -DTSDTPLCQLSQGIYLTNRYMSISLVTAIAVDRYVAVRHPLRARGLRSPRQAAAVCAVL 140 104 WPFGDT-LCKISGTAFLTNIYGSMLFLTCISVDRFLAIVYPFRSRTIRTRRNSAIVCAGV 162 Š

WVLVIGSLVARWILGIQEGGF-----CPR----STRHNFNSMRFPLLGFYL 182 141 ò

셤

163 WILVLSG------GISASLFSTINVNNATTTCFEGLSKRVWKTYLSKITIFIEVVGFII 셤

PLAVVVFCSLKVVTALAORPPTDVGQAEAT-RKAARMVWANLLVFVVCFLPLHVGLTVRL 241 183 Š 셤 242 AVGWNAC--ALLETIRRALY-ITSKLSDANCCLDAICYYYMAKEFQEASALAVAPRAKAH 298 ò

274 LVRSQAITNCFLERFAKIMYPITLCLATLNCCFDPFIXYFTLESFQKSFYI-----NAH 327 원

ŝ g

ISO241
G protein-coupled receptor 6H1 - chicken
N;Alternate names: purinoceptor 6H1
C;Species: Gallus gallus (chicken)
C;Species: Ja-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 09-Jul-2004
C;Accession: ISO241; JC4618

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C; Superfamily: G protein-coupled receptor 4
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                                                                                Query Match
Best Local Similarity
Matches 95; Conserv
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C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 09-Jul-2004
C;Accession: I69202
R;Nomura, H.; Nielsen, B.W.; Matsushima, K.
Int. Immunol. S; 1239-1249; 1993
A;Accession: I69202
A;A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A MOLECULE type: mRNA
A, Residues: 1-308 ~WEB>
A, Crosser-references: UNIPARC: UPI0000055A6B; GB: L06109; NID: g304383; PIDN: AAB06587.1; PID: A, Experimental source: T-cells
C, Comment: This receptor plays a role in T-cell activation.
C, Genetics:
A, Gene: p2x8
C, Superfamily: ATP receptor P2u
C, Keywords: G protein-coupled receptor; transmembrane protein
C, Keywords: G protein-coupled receptor; transmembrane predicted <TM1>
F; 15-40, Domain: transmembrane #status predicted <TM2>
F; 15-109, Domain: transmembrane #status predicted <TM3>
F; 13-153, Domain: transmembrane #status predicted <TM5>
F; 177-201, Domain: transmembrane #status predicted <TM5>
F; 227-248, Domain: transmembrane #status predicted <TM5>
                                                                                                                                                                                                                                                                                                              A/Cross-references: UNIPROT:P32250; UNIPARC:UPI0000055A6B; GB:L06109; NID:g304383; PIDN:R;Webb, T.E.; Kaplan, M.G.; Barnard, E.A.
R;Webb, T.E.; Kaplan, M.G.; Barnard, E.A.
Biochem. Biochyar. Res. Commun. 219, 105-110, 1996
A;Title: Identification of 6H1 as a P2Y purinoceptor: P2Y5.
A;Reference number: JC4618; MUID:96190677; PMID:8619790
A;Accession: JC4618
R;Kaplan, M.H.; Smith, D.I.; Sundick, R.S.
J. Immunol. 151, 628-636, 1993
A;Title: Identification of a G protein coupled receptor induced in activated T cells.
A;Reference number: ISO241; MUID:93329058; PMID:8393036
A;Accession: ISO241
A;Accession: Iso141
A;Reture: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-308 «KAP»
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intron 17 purinergic receptor P2YS - human
NiAlternate names: G-protein coupled receptor
C;Species: Homo sapiens (man)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C;Accession: 109508
R;Bohm, S.K.; Trumpp, A.; Khitin, L.M.; Kong, W.; Payan, D.G.; Bunnett, N.W.
submitted to the EMBL Data Library, April 1997
A;Description: The human purinergic receptor P2YS is encoded in intron 17 of the retinoble A;Accession: 709508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Reaidus: 1-344 <BOH>
A;Reaidus: 1-344 <BOH>
A;Cross-references: UNIPROT:P43657; UNIPARC:UP1000005041B; EMBL:AF000546; NID:g2232068; E
                                                                         17
                                                                                                                                                                                                                                                                                                                                                                                                                                                         142 VLVIG---SLVARWLLGIQBG--GFCFR-STRHNF--NSMRFPLLGFYLPLAVVVFCSLK 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    194 VVTALAQRPPTDVGQAEATRKAARMVWANLLVFVVCFLPLHVGLTVRLAVGW-----N 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           211 IIWSLRQR----QMDRHAKIKRAITFIMVVAIVPVICFLP----SVVVRIRIFWLLHTSGTQ 264
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             176 TWKTYLSRIVIFIEIVGFFIPLILLAVICSSMVLKTLTK--PVTLSRSKINKTKVLKMIFV 233
                                                                                                                                                                                                                                                                             82 DTSDTPLCQLSQGIYLTNRYMSISLVTAIAVDRYVAVRHPLRARGLRSPRQAAAVCAVLW 141
                                                                                                                                                                                  34 IGLEFIFGLIGNGLALMIFCFFHIKSWKSSRIFLFNLAVADFLLIICLFFVMDYYVRRSDW 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             65
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                                                                                                                                                                                                                                                                                                                       94 NPGDIP-CRLVLFMFAMNRQGSIIFLTVVAVDRYFRVVHPHHALNKISNWTAAIISCLLW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6 SSHCFYNDSFKYTLYGGMFSMYFVLGLVSNCVALXIFICVLKVRNETTTYMINLAMSDLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         222 NLLVFVVCFLPLHVGLTVRLAVGWNA---CALLETIRRALYITSKLSDANCCLDAICYYY
                                                                                                                                            27 LGVLLVLGLLLNSLALWVFCCRMQQWTETRIYMTNLAVADLCLLCTLPPVL----HSLR
                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SSDLTWPPAIKLGFYAYL-GVLLVLGLLLNSLALWVFCCRMQQWTETRIYMTNLAVADLC
                                                                         29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               43;
       Length 387;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 22.3%; Score 360.5; DB 2; Length 3
Best Local Similarity 29.2%; Pred, No. 1e-25;
Matches 90; Conservative 68; Mismatches 107; Indels
                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Map position: 13
C;Superfamily: ATP receptor P2u
C;Keywords: G protein-coupled receptor; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         247 ACALLETIRRALYITSKLSDANCCLDAICYYYMAKEF 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                265 NCEVYRSVDLAPFITLSFTYMNSMLDPVVYYFSSPSF 301
ch 22.8%; Score 368.5; DB 2; Similarity 34.3%; Pred. No. 2.16-26; 95; Conservative 48; Mismatches 105;
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R;Webb, T.E.; Simon, J.; Krishek, B.J.; Bateson, A.N.; Smart, T.G.; King, B.F.; Burnstor FBBS Lett. 324, 219-225, 1993
A;Title: Cloning and functional expression of a brain G-protein-coupled ATP receptor. A;Reference number: S33733; MUID:93285340; PMID:8508924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A,Molecule type: mrNA
A,Residues: 1-362 <MRBD.
A,Residues: 1-362 <MRBD.
A,Cross-references: UNIPROT: P34996; UNIPARC: UPI0000405D4; EMBL: X73268; NID: G395084; PI:
C,Superfamily: ATP receptor P2u
C,Reywords: G protein-coupled receptor; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      157 QEGG--FCFRSTRHNF-----NSMRFPLLGFYLPLAVVVFCSLKVVTALAQRPPTDVGQ 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      209 AEATRKAARMVWANLLVFVVCFLPLHVGLTVRLAVGWN-----ACALLETIRRALVITSK 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241 SPLRRKSIYLVIIVLTVFAVSYLPFHVMKTLNLRARLDFQTPQMCAFNDKVYATYQVTRG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                              45 FCCRMQQWTETRIYMTNLAVADLCLLCTLPFVLHSLRDTSD----TPLCQLSQGIYLTNR 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRHN-------FNSMRFPLLGFYLPLAVVVFCSLKVVTALAQRPP--TDVGQAE 210
                                                                                                                                                                                                                                                                                                                                                    104
                                                                                                                                      105 SLVTAIAVDRYVAVRHPLRARGLRSPROAAVCAVLWVLVIGSLVARWLLGIQEGEFCFR 164
                                                     61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            G protein-coupled receptor - chicken
C;Species: Gallus gallus (chicken)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C;Accession: S33733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATRKAARMVWANLLVFVVCFLPLHVGLTVRLAVGW--NACALLETIRRALYITSKLSDAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                101 YMSISLVTAIAVDRYVAVRHPLRARGLRSPRQAAAVCAVLWVLVIGSLVARWLL----GI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MNGTY-----GLLLNSLALWV
                                                                                                       49 MOGWTETRIYMTNLAVADLCLLCTLPFVLHSLRDTSDTP----LCQLSQGIYLTNRYMSI
                           9 NSTINGTWEGD------ELGYKCRFNEDPRYVLLPVSYGVVCVLGLCLNVVALXIFLCR
2 NGTYNTCGSSDLTWPPAIKLGF-----YAYL----GVLLVLGLLLNSLALWVFCCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63; Mismatches 134; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LSDANCCLDAICYYYMAKEFQEASALAVAPRAKAHKSQDSL 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CCLDAICYYY------MAKEFOEASALAVAPRAK 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 28.28
Matches 96; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A,Status: preliminary
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                                                                                                       Cross-references: UNIPROT:P35383; UNIPARC:UPI0000027DFF; GB:L14751; NID:g309457; PIDN:
Superfamily: ATP receptor P2u
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C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C;Accession. A47556
R;Lustig, K.D.; Shiau, A.K.; Brake, A.J.; Julius, D.
Proc. Natl. Acad. Sci. U.S.A. 90, 5113-5117 1993
A;Titler Expression cloning of an ATP receptor from mouse neuroblastoma cells. A;Accession. A47556
A;Accession. A4756
A;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    236 KAARMAVVVAAVEVISELPEHITKTAYLAVRSTPGVSCPVLETEAAAYKGTRPFASANSV 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51 QWTETRIYMTNLAVADLCLLCTLPFVLHSLRDTSDTPL----CQLSQGIYLTNRYMSISL 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                107 VTAIAVDRYVAVRHPLRARGLRSPRQAA-AVÇAVLWVLVIGSLVARWLL---GIQEG-GF 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CF-----RSTRHNFNSMRPPLLGFYLPLAVVVPCSLKVVTALAQR--PPTDVGQAEATR 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 NGTY-----NTCGSSD----LITWPPAIKLGFYAYLGVLLVLGLLLNSLALWVFCCRMQ 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 S NGTIQAPGLPPTTCVYREDPKRLLLPPV-----YSVVLVVGLPLNVCVIAQICASRR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 328;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 19.8%; Score 319; DB 2; Length 32 Best Local Similarity 30.6%; Pred. No. 6.6e-22; Matches 96; Conservative 48; Mismatches 130; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             || | :|: ::|:
LDPILFYFTQQKFR 309
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             : | :
294 TSDTIQNS 301
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A;Accession: A55559
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Rossidues: 1-364 <MAA>
A;Cossidues: 1-364 <MAA>
A;Cross-references: UNIPARC:UDI000002A4FC; GB:L27594
R;Hess, J.F.; Borkowski, J.A.; Young, G.S.; Strader, C.D.; Ransom, R.W.
B;chem Biophys: Res. Commun. 184, 260-268, 1992.
A;Title: Cloning and pharmacological characterization of a human bradykinin (BK-2) receptive for the parameter of the parame
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Residues: 1.364 <HES>
A;Cross-references: UNIPARC:UPI000002A4FC; GB:M88714; NID:g1387999; PIDN:AAB02793.1; PID
    Reference number: A55559; MUID:95137582; PMID:7835885
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Best Local Similarity 27.6
Matches 89; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Accession: JQ1488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gene: GDB:BDKRB2
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C;pgecies: Home sapiens (man)

C;pate: 17-Jul-1992 #sequence revision 17-Jul-1992 #text_change 09-Jul-2004

C;pate: 17-Jul-1992 #sequence revision 187, 1306-1313, 1992

A;Pateles: Biophys. Res. Commun. 187, 1306-1313, 1992

A;Accession: JH0712

A;Accession: JH0712

A;Accession: JH0712

A;Accession: JH0712

A;Accession: JH0712

A;Accession: Adf022

A;Accession:
G protein-coupled receptor - human
G protein-coupled receptor - human
G protein-coupled receptor - human
C;Species Bome as agiens (man)
C;Species Bome as agiens (man)
C;Species Bome as agiens (man)
C;Accession: S68679
R;Stam, N.J.; Klomp, J.; van de Heuvel, M.; Olijve, W.
FEBS Lett. 384, 260-264, 1996
A;Title: Molecular cloning and characterization of a novel orphan receptor (P(2P)) expre
A;Reference number: 868679; MUD:96197801; PMID:8617367
A;Reference number: 868679
A;Reference number: B68679
A;Reference number: B68679
A;Residues: DNA
A;Residues: 1-365 <STA>
A;Residues: 1-365 <STA>
Crossa-references: UNIPROT:P51582; UNIPARC:UPIO00002E776; EMBL:X96597; NID:g1296631; PI
C;Superfamily: ATP receptor P2u
C;Keywords: G protein-coupled receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LIETIRRALYITSKLSDANCCLDAICYYYMAKEFQE-------ASALAVAP 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---LCQLSQGIYLTNRYMSISLVTAIAVDRYVAVRHPLRARGLRSPRQAAAVCAVLWVLV 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     145 IGSLVAR-WILGIQEGG---FCFRSTR----H--NFNSMRFPLLGFYLPLAVVVFCSLK 193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              44 VVFVLGLGLNAPTLWLFIFRLRPWDATATYMFHLALSDTLYVLSLPTLIXYXAAHNHWPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VLLVLGLLLNSLALWVFCCRMQQWTETRIYMTNLAVADLCLLCTLPFVLHSLRDTSDTP-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 Similarity 29.1%;
93; Conservative 5
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Matches 93; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        88
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A;Crose-references: GDB:135713; OMIM:113503
A;Amap position: 14q32.1-14q32.2
A;Introns: #etatus absent
A;Introns: #etatus absent
C;Superfamily: vertebrate rhodopsin
C;Superfamily: vertebrate rhodopsin
C;Superfamily: vertebrate receptor; glycoprotein; phosphoprotein; transmembrane #status predicted <TM1>
F;34-56/Domain: transmembrane #status predicted <TM2>
F;66-92/Domain: transmembrane #status predicted <TM3>
F;104-127/Domain: transmembrane #status predicted <TM3>
F;105-221/Domain: transmembrane #status predicted <TM5>
F;35-221/Domain: transmembrane #status predicted <TM5>
F;34-26/Domain: transmembrane #status predicted <TM5>
F;34-26/Domain: transmembrane #status predicted <TM5>
F;34-27-309/Domain: transmembrane #status predicted <TM5>
F;34-27-309/Domain: transmembrane #status predicted <TM7>
F;34-27-309/Domain: transmembrane #status predicted <TM7>
F;34-28-309/Domain: transmembrane (Thr) (covalent) (by protein kinase A) #status predicted F;316/Binding site: phosphate (Thr) (covalent) (by protein kinase A) #status predicted F;316/Binding site: phosphate (Ser) (covalent) (by protein kinase A) #status predicted
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C;Date: 30-Sep-1992 #text_change 09-Jul-2004
C;Accession: A41283; A55079; S47529
C;Accession: A41283; A55079; S47529
R;McBachern, A.E.; Shelton, E.E.; Bhakta, S.; Obernolte, R.; Bach, C.; Zuppan, P.; Fujis: Proc. Natl. Acad. Sci. U.S.A. 88, 7724-7728, 1991
A;Title: Expression cloning of a rat B-2 bradykinin receptor.
A;Reference number: A41283; MUID:91352062; PMID:1715575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        53 TETRIYMTNLAVADLCLLCTLPFVLHSLRDTSD----TPLCQLSQGIYLTNRYMSISLVT 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63 TVAEIYLGNLAAADLILACGLPFWAITISNNFDWLFGETLCRVVNAIISMNLYSSICFLM 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    109 AIAVDRYVAVRHPIRARGIRSPROAAAVCAVLW--VLVIGS--LVARWILGIOEGGFCFR 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----FNSMRFPLLGFYLPLAVVVFCSLKVVTALAQRPPTDVGQA 209
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         :|||:
11 INGTFAQSKCPQVEWINGWINTIQPP------FIMVLFVLATLENIFVLSVPCLHKSSC 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  179 ---HNVTACVISYPSLIWEVFTNMLLNVVGFLLPLSVITFCTMQIMQVLRNNEMQKFKEI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19.4%; Score 312.5; DB 2; 27.6%; Pred. No. 2.9e-21; tive 54; Mismatches 128;
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A, Molecule type: mRNA
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Similarity 28.2
81; Conservative
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nes 89; Conserv
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Best Local S
Matches 81
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A, Residues: 1-366 < WAN.

A, Residues: 1-366 < WAN.

A, Residues: 1-366 < WAN.

A, Cross-references: UNIPARC: UPI00001708A1; EMBL: L26173; NID: 9476749; PIDN: AAA62492.1; PI
C, Comment: This G protein-coupled receptor binds the nonapeptide bradykinin.
C; Superfamily: vertebrate rhodopsin
C; Superfamily: vertebrate splicing; G protein-coupled receptor; glycoprotein; lipoprotein;
F; 31-48/Domain: transmembrane #status predicted < TM1>
F; 79-96/Domain: transmembrane #status predicted < TM2>
F; 79-96/Domain: transmembrane #status predicted < TM3>
F; 70-125/Domain: transmembrane #status predicted < TM5>
F; 710-125/Domain: transmembrane #status predicted < TM6>
F; 710-125/Domain: transm
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A;Residues: 1-366 <MCE>
A;Residues: 1-366 <MCE>
A;Residues: 1-366 <MCE>
A;Crose=references: UNIPARC:UPI00001708A1; GB:M59967
B;Crose=references: UNIPARC:UPI00001708A1; Ganten, D.; Bader, M.
J. Biol. Chem. 269, 26920-26925, 1994
A;Title: Molecular structure and expression of rat bradykinin B2 receptor gene. Evidence A;Reference number: A55079; MUID:95014558; PMID:7929432
A;Accession: A55079
A;Retence president structure and with conceptual translation
A;Retence president structure and with conceptual translation
A;Residues: 1-75, 'A', 77-366 <PES>
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Biochim. Biophys. Acta 1219, 171-174, 1994
A;Title: Molecular cloning and sequence analysis of rat bradykinin B(2) receptor gene. A;Reference number: S47529; MUID:94368850; PMID:8086459
A;Accession: S47529
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  platelet-activating factor receptor - guinea pig
C;Species: Cavia porcellus (guinea pig)
C;Apecies: Cavia porcellus (guinea pig)
C;Accession: S13638
R;Honda, Z.; Nakamura, M.; Miki, I.; Minami, M.; Watanabe, T.; Seyama, Y.; Okado, Nature 349, 342-346, 1991
A;Title: Cloning by functional expression of platelet-activating factor receptor fakeerence number: S13638, MUID:91101726; PMID:1846231
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|----ERAVDIVTQISSYVAYS 298
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VRHPLRARGLRSPRQAAAVCAVLW--VLVIGS--LVARWLLGIQEGGFCFRSTRHN---- 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----FNSMRPPLLGFYLPLAVVVFCSLKVVTALAQRPPTDVGQAEATRKAARM 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           187 VIVYPSRSWEVFTNMLINLVGFILIPLSIITFCTVRIMQVLRNNEMKKFKEVQTEKKATVL 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VMANLLVFVVCFLPLHVG--LTVRLAVG-----WNACALLETIRRALYITSKLSD----A 267
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14 NGTFSEVNCPDTEWWSWIANALQAPFLWVLFLIAALENIFVLSVFCLHKTNCTVABIYLGN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19.4%; Score 312.5; DB 328.1%; Pred. No. 2.9e-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             268 NCCLDAICYYYMAKEFQEAS 287
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nes 907 Conserv
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A;Status: preliminary
A;Molecule type: mENA
A;Residues: 1-342 <HON>
A;Residues: 1-342 <HON>
A;Cross-references: UNIPROT:P21556; UNIPPARC:UPI00001311EE; GB:X56736; NID:949442; PIDN:C
A;Note: the species of guinea pig is not identified; in GenBank entry CCPAFREC, release
C;Superfamily: ATP receptor P2u
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CjAccession: A54946

CjAccession: A54946

Figure C. C. B.; Millivan, D.M.; Paradiso, A.M.; Lazarowski, E.R.; Burch, L.H.; Olsen, J.C. Proc. Natl. Acad. Sci. U.S.A. 91, 3275-3279, 1994

A;Title: Cloning and expression of a human P-2U nucleotide receptor, a target for cystic A;Title: Cloning and Safeteneous number: A54946; MUID:94211846; PMID:8159738

A;Accession: A54946

A;Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                               141
                                                                                                                                                                                                                                                                                                                                                                                                                                            245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    201 LILECNLVIIHTLERQPVKQORNAEVRRRALWMVCTVLAVFVICEVPHHM-----VQLPW 255
                                                                                                                                                                                                                                                                                                                                                        82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P-20 nucleotide receptor - human
C;Species: Homo sapiens (man)
C;Date: 11-Nov-1994 #sequence_revision 11-Nov-1994 #text_change 17-Mar-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 88 ----LCQLSQGIYLTNRYMSISLVTAIAVDRYVAVRHPLRARGLRSPRQAAAVCAVLWVL
                                                                                                                                                                                                                                                                                                                                 GVLLVLGLLLNSLALWVFCCRMQQWTETRIYMTNLAVADLCLLCTLPFVLHSLRDTSDTP
                                                                                                                                                                                                                                                                                                                                                                                                               84 SDTP--LCQLSQGIYLTNRYMSISLVTAIAVDRYVAVRHPLRARGLRSPRQAAAVCAVLW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VLVIGSLVARWILGIQE-----GGFCFRSTRHNFNSMRFPL-----LGFYLPLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        186 VVVFCSLKVVTALAQRPPTDVGQAEATRKAARMVWANLLVFVVCFLPLHVGLTVRLAVGW
                                                                                                                                                                                                                                                                                                    29 VLLVLGLLLNSLALWVFCCRM---QOWTETRIYMTNLAVADLCLLCTLP--FVLHSLRDT
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A;Residues: 1.375 < PAR>
A;Cross-references: UNIPARC:UPI0000145104; GB:U07225
A;Note: parts of this sequence were confirmed by protein sequencing
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TLAELGMWPSSNHQAINDAHQVTLCLLSTNCVLDPVIYCFLTKKFRK 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     246 NACAL-----LETIRRALYITSKLSDANCCLDAICYYYMAKEFQE 285
                                                                                                                                                                                         Length 342;
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A,Cross-references: GDB:362713; OMIM:600041
A,Map position: 11q13.5-11q14.1
C,Superfamily: ATP receptor P2u
C,Superfamily: ATP receptor P2u
C,Keywords: G protein-coupled receptor; transmembrane
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                                                                                                                                                                                         19.2%; Score 310; DB 2; I 28.2%; Pred. No. 4.7e-21; ive 58; Mismatches 110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     144 VIGSLVARWLIGIQEGGFCFRSTRHNFNSMRFPL-
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A57641
G protein-coupled receptor 4 - human
C; Species: Homo sapiens (man)
C; Accession: A57641
R; Mahadevan, M.S.; Baird, S.; Bailly, J.E.; Shutler, G.G.; Sabourin, L.A.; Tsilfidis, C. A; Tille: Isolation of a novel G protein-coupled receptor (GPR4) localized to chromosome A; Reference number: A57641; MUID:96129306; PMID:8595909
A; Recension: A57641; MUID:96129306; PMID:8595909
A; Recension: A57641
A; Residues: L-362 < ANA+>
A
                                                                                                                                                                                               RESULT 13
I53033
G protein-coupled receptor - human
C; Species: Homo sapiens (man)
C; Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C; Accession: 153033
R; Heiber, M.; Docherty, J.M.; Shah, G.; Nguyen, T.; Cheng, R.; Heng, H.H.Q.; Marchese, R. M.; Docherty, J.M.; Shah, G.; Nguyen, T.; Cheng, R.; Heng, H.H.Q.; Marchese, R. A; Reference number: 13933 MUD:95134353; PMID:7832990
A; Reference number: 153033 MUD:95134353; PMID:7832990
A; Reference number: 153033
A; Restue: prefilminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-354 <RES
A; Residues: 1-354 <RES
A; Residues: G protein-coupled receptor
C; Superfamily: G protein-coupled receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SLIAIVLVCFAPYHVLLLSRSAIYLGRPWD-CGFEERVFSAYHSSLAPTSLNCVADPILY 286
207 AVPFAVILVCYVLMARRLL-KPAYGTSGGLPRAKRKSVRTIAVVLAVFALCFLPFHVTRT 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : ||::||| :|||| :|||| 56 LMNLXIADAPLHHDNWIHGPGSCKLFGFIFYTNIYISIAPLCCISVDR 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YVAVRHPLRARGLRSPRQAAAVCAVLWVLVIGSLVARWLLGIQEGGFCFRST-RHNFNSM 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      :||:
171 KFPMEGWVAMMILYRVFVGFLPPWALMILSYRGILRAVRGSVST---ERQEKAKIKRLAL 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          221 ANLLVFVVCFLPLHVGLTVRLAV----GWNACALLETIRRALYITSKLSDANCCLDAICY 276
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                                                           239 VRLAVGW--NACALLETIRRALYITSKLSDANCCLDAICYY 277
                                                                                                                    266 LYYSFRSLDLSCHTLNAINMA-YKVTRLASANSCLDPVLYF 305
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Best Local S:
Matches 93,
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A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-352 cMAC>
A;Residues: 1-352 cMAC>
A;Cross-references: UNIPROT:P48748; UNIPARC:UPI0000126ABF; EMBL:U20507; NID:g1041820; PII
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    a rabbit bradykinin B(1) recepto
                                                                   11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 194 HEAWHWLRMVELNLIGFLLPLAAILFFNCHILASLRRRGERVPSRCGGPRDSKSTA-LIL 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    221 ANLLVFVVCFLPLHVGLTVRL----AVGWNACALLETIRRALYITSKLSDANCCLDAIC 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               253 TLVASFLVCWAPYHFRAFLECLWQVHAIG--GCFWEEFTDLGLGLSNFSRFVNSCLNPVI 310
                                                                                                                                                                                                                                                                         114
                                                                                                                                                                                                                                                                                                             116 YLAVAHPLRPARLRRVKTAVAVSSVVWATBLGANSAP--LPHDE---LPRDRYNHTPCPE 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YVAVRHPLRARGLRSPRQAAAVCAVLWVLVIGSLVARWLLGIQEGGFCFRST-RHNFNSM 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RFPL------LGFYLPLAVVVFCSLKVVTALAQRPFTDVGQAEATRKAARMVW 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                171 KFPMEGWVAWMNLYRVFVGFLFPWALMLLSYRGILRAVRGSVST---ERQEKAKIKRLAL 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LCLLCTLPFVLHSLRDTSDTP----LCQLSQGIYLTNRYMSISLVTAIAVDRYVAVRHPL 122
                                                                                                                                      28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         bradykinin B1 receptor - rabbit
C;Species: Oryccolagus cuniculus (domestic rabbit)
C;Date: 24-Aug-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C;Date: 260024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       221 ANLLVFVVCFLPLHVGLTVRLAV----GWNACALLETIRRALYITSKLSDANCCLDAICY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SLIAIVLVCPAPYHVILLSRSAIYLGRPWD-CGFERRVFSAYHSSLAFTSLNCVADPILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24 SCSGAPDAWDLLHRL-LPTFIIAIFTLGLLGNSFVLSVFLLARRRLSVAEIYLANLAASD
                                                                                                                                                                                                                                                                         MINLAVADLCLLCTLP----FVLHSLRDTSDTPLCQLSQGIYLTNRYMSISLVTAIAVDR
                                                                                                                                   2 NGTYNTC---GSSDLTWPPAIKLGFYAYLGVLLVLGLLLNSLALWVFCCRMQQWTBTRIY
                                                                                                                                                                                                   3 NHTWEGCHVDSRVDHLPPPSL----YIPVIGV-GLPTNCLALWAAYRQVQQRNELGVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7 TCGSSDLTWPPAIKLGFYAYLGVLLVLGLLLNSLALWVFCCRMQQWTBTRIYMTNLAVAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              123 RARGLRSPRQAAAVCAVLWVLVIGSLVARWLLGIQEGGFCFRSTR-------
                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    52; Gaps
                                                                   41;
   Length 362;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 352;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
18.9%; Score 305; DB 2; Length 35;
Best Local Similarity 26.6%; Pred. No. 1.4e-20;
Matches 89; Conservative 62; Mismatches 131; Indels
                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Superfamily: vertebrate rhodopsin;Keywords: G protein-coupled receptor; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R.MacNeil, T., Bierilo, K.K.; Menke, J.G.; Hess, J.F.
Biochim. Biophys. Acta 1264, 223-228, 1995
A.Title: Cloning and pharmacological characterization of
A.Reference number: S60024; MUID:96085127; PMID:7495867
Query Match 18.9%; Score 305.5; DB 2; Best Local Similarity 31.0%; Pred. No. 1.3e-20; Matches 93; Conservative 48; Mismatches 118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           276 YYYMAKEP-----QEASALAVAPRAKAHKSQ 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | :: : | : : : | :: | 344
```

Job time : 28.5 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd
```

 protein search, using sw model OM protein February 9, 2006, 00:55:13 Run on:

; Search time 26.5 Seconds (without alignments) 1121.924 Million cell updates/sec

Title: Perfect score: Sequence:

US-10-083-168-85 1615 1 MNGTYNTCGSSDLTWPPAIK......AVAPRAKAHKSQDSLCVTLA 309

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

summaries Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 su

PIR 80:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

|               |       |                |        |    | SUMMARIES |                    |
|---------------|-------|----------------|--------|----|-----------|--------------------|
| Result<br>No. | Score | Query<br>Match | Length | DB | ΔI        | Description        |
| 1             | 400   | 24.8           | 370    | 2  | JC5549    | heptahelical P2Y5- |
| 10            | 369.5 | 22.9           |        | N  | 169202    | G protein-coupled  |
| e             | 367.5 | 22.8           |        | 7  | I50241    | G protein-coupled  |
| 4             | 359.5 | 22.3           |        | ~  | T09508    | intron 17 purinerg |
| Ŋ             | 317   | 19.6           |        | ~  | A47556    | ATP receptor P2u - |
| 9             | 316   | 19.6           |        | 7  | S33733    | G protein-coupled  |
| 7             | 315.5 | 19.5           | 365    | ~  | 868679    |                    |
| 80            | 314   | 19.4           |        | 7  | I55450    |                    |
| O             | 311.5 | 19.3           |        | 7  | I53033    |                    |
| 10            | 311.5 | 19.3           |        | 7  | A57641    | G protein-coupled  |
| 11            | 311.5 | 19.3           |        | 7  | JQ1488    | bradykinin B2 rece |
| 12            | 311.5 | 19.3           |        | Н  | CORTB2    | bradykinin recepto |
| 13            | 309   | 19.1           |        | ~  | S13638    | platelet-activatin |
| 14            | 308.5 | 19.1           | 362    | ~  | B57641    |                    |
| 15            | 307.5 | 19.0           |        | ~  | S68207    | G protein-coupled  |
| 16            | 306.5 | 19.0           |        | N  | A54946    | P-2U nucleotide re |
| 17            | 303   | 18.8           |        | ~  | A40191    | platelet-activatin |
| 18            | 303   | 18.8           |        | ~  | S60024    | bradykinin B1 rece |
| 19            | 300.5 | 18.6           |        | N  | JC4162    | P2Y receptor - bov |
| 20            | 296.5 | 18.4           |        | 7  | JC4737    | G protein-coupled  |
| 21            | 292   | 18.1           | 341    | 7  | S43252    | platelet-activatin |
| 22            | 288   | 17.8           |        | ~  | JC2543    | angiotensin II rec |
| 23            | 286.5 | 17.7           |        | 7  | A43113    | chemokine (C-C) re |
| 24            | 286   | 17.7           | 328    | 7  | JC4800    | P2Y6 receptor - hu |
|               | 284.5 | 17.6           |        | ~  | B45680    | G protein-coupled  |
| 26            | 282   | 17.5           | 341    | 7  | 863666    | platelet activatin |
| 27            | 280.5 | 17.4           | 366    | 7  | 149519    | bradykinin B2 rece |
| 28            | 279.5 | 17.3           | 361    | 0  | JC5653    | G protein-coupled  |
| 29            |       | 17.2           | 363    | 8  | 157955    | somatostatin recep |

| somatostatin recep | angiotensin II rec | angiotensin II rec | somatostatin recep | G protein-coupled | macrophage inflamm | thrombin receptor | G protein-coupled | HHRF3 protein - hu | somatostatin recep | G protein-coupled | angiotensin II rec | G protein-coupled | somatostatin recep | somatostatin recep | somatostatin recep |
|--------------------|--------------------|--------------------|--------------------|-------------------|--------------------|-------------------|-------------------|--------------------|--------------------|-------------------|--------------------|-------------------|--------------------|--------------------|--------------------|
| JN0763             | A49092             | 148261             | I57940             | S68208            | I49339             | 151667            | T09353            | одвер3             | A46226             | JC5067            | JC2134             | JC5068            | A41795             | C41795             | A39297             |
| ~                  | N                  | ~                  | ~                  | N                 | N                  | α                 | ~                 | -                  | 7                  | 7                 | ~                  | ~                 | ~                  | ~                  | ~                  |
| 64                 | 363                | 363                | 363                | 365               | 355                | 420               | 354               | 323                | 418                | 355               | 359                | 369               | 391                | 391                | 391                |
| m                  | •••                |                    |                    |                   |                    |                   |                   |                    |                    |                   |                    |                   |                    |                    |                    |
|                    |                    | 17.0               | 17.0               | 16.9              | 16.7               | 16.7              | 16.7              | 16.5               | 16.5               | 16.4              | 16.2               | 16.2              | 16.2               | 16.2               | 16.2               |
|                    |                    |                    | 274 17.0           |                   | 270.5 16.7         |                   |                   |                    | 267 16.5           |                   | 261.5 16.2         |                   |                    |                    |                    |

## ALIGNMENTS

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| Θ | Ş |

heptahelical P2Y5-like receptor - human

C;Species: Homo sapiens (man) C;Date: 02-Sep\_1997 #sequence\_revision 05-Sep-1997 #text\_change 09-Jul-2004

CjAccession: JC5549
R;Janssens, R; Boeynaems, J.M.; Godart, M.; Communi, D.
Rsjanssens, R.; Boeynaems, J.M.; Godart, M.; Communi, D.
Biochem, Biophys. Res. Commun. 236, 106-112, 1997
A;Title: Cloning of a human heptahelical receptor closely related to the P2YS receptor.
A;Reference number: JC5549; MUID:97366605; PMID:9223435

A;Accession: JC5549
A;Molecule type: DNA
A;Residues: 1-370 <JAN>
A;Residues: 1-370 <JAN>
A;Cross-references: UNIPROT: Q99677; UNIPARC: UPI000016A4CA; DDBJ:AF005419; NID:g2240034; C;Superfamily: ATP receptor P2u

Query Match 24.8%; Score 400; DB 2; Length 370; Best Local Similarity 34.0%; Pred. No. 1.3e-29; Matches 105; Conservative 58; Mismatches 104; Indels 42;

44 AVYSVVFILGLITHSVSLEVFCFRRKARSETAIFITHLAVSDLLFVCTLPFKIFYNFNRH 103 25 AYLGVILVIGLILNSLALWVFCCRMQQWTETRIYMTNLAVADLCLLCTLPF-VLHSLR-à

셤 ò

q 141 WVLVIGSLVARWLLGIQEGGF-----CFR-----STRHNFNSMRFPLLGFYL 182 ઠે

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183 PLAVVVFCSLKVVTALAQRPPTDVGQAEAT-RKAKRMVWANLLVFVVCFLPLHVGLTVRL 241 216 PLILAVSCSSVVLRTL--RKPATLSQIGTNKKKVLKMITVHMAVFVVCFVPYNSVLFLYA 273 셤 ઠે

242 AVGWNAC--ALLETIRRALY-ITSKLSDANCCLDAICYYYMAKEFOEASALAVAPRAKAH 298 ઠે

299 KSQDSLCVT 307

ò a

328 IRMEŠĽFKŤ 336

RESULT 2

169202 G protein-coupled receptor HM74 - human C;Species: Homo sapiens (man) C;baceiss: Homo sapiens (man) C;bacession: 162202 R;Nomura, H.; Nielsen, B.W.; Matsushima, K.

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F;269-292/Domain: transmembrane #status predicted <TM7>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A, Map position: 13
C, Superfamily: ATP receptor P2u
                                                                                                                                                     91; Conservative
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                                                                                                                 Similarity
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A.Residues: 1-308 <WEB>
A.Residues: 1-308 <WEB>
A.Residues: 1-308 <WEB>
A.Cross-references: WINDAC: UP10000055A6B; GB:L06109; NID:g304383; PIDN:AAB06587.1; PID:
A.Faxperimental source: T-cells
C;Comment: This receptor plays a role in T-cell activation.
C;Gometics:
A;Genetics:
A
A,Title: Molecular cloning of cDNAB encoding a LD78 receptor and putative leukocyte chem A,Title: Molecular cloning of cDNAB encoding a LD78 receptor and putative leukocyte chem A,Aceference number: I54751; MUID:94092629; PMID:7505609
A,Aceference number: I54751; MUID:94099; PMID:7505609
A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: mRNA
A,Residues: 1-387 <RES>
A,Cross-references: UNIPROT:P49019; UNIPARC:UPI0000043G3C; GB:D10923; NID:9219866; PIDN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: mRNÅ
A;Residues: 1-308 cKAP>
A;Residues: 1-308 cKAP>
A;Residues: 1-308 cKAP>
A;Cross-references: UNIPROT: P32220; UNIPARC: UPI0000055A6B; GB:L06109; NID:G304383; PIDN:
R;Webb, T.E.; Kaplan, M.G.; Barnard, E.A.
Biochem. Biophys. Res. Commun. 219, 105-110, 1996
A;Title: Identification of 6H1 as a P2Y purinoceptor: P2Y5.
A;Reference number: JC4618; MUID:96190677; PMID:8619790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  G protein-coupled receptor 6H1 - chicken
NyAlternate names: purinoceptor 6H1
C;Species: Gallus (chicken)
C;Date: 13-Sep-1996 #text_change 09-Jul-2004
C;Accession: 150241; U76618
R;Kaplan, M.H.; Smith, D.I.; Sundick, R.S.
J. Immunol. 151, 628-636, 1993
A;Title: Identification of a G protein coupled receptor induced in activated T cells.
A;Reference number: I50241; MUID:93329058; PMID:8393036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94 NFGDIP-CRLVLFMFAMNRQGSIIFLTVVAVDRYFRVVHPHALNKISNWTAAIISCLLW 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       142 VLVIG---SLVARWLLGIQEG--GFCFR-STRHNF--NSMRFPLLGFYLPLAVVVFCSLK 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          194 VVTALAQRPPIDVGQAEATRKAKR---MVWANLLVFVVCFLPLHVGLTVRLAVGW---- 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     211 IIWSLRQR-----QMDRHAKIKGAITFIMVVAIVFVICFLP---SVVVRIRIFWLLHTS 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    82 DTSDTPLCQLSQGIYLTNRYMSISLVTAIAVDRYVAVRHPLRARGLRSPRQAAAVCAVLW 141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27 LGVLLVLGLLLNSLALWVFCCRMQQWTETRIYMTNLAVADLCLLCTLPFVL-----HSLR
                                                                                                                                                                                                                                                                                                                                                                                                                               22.9%; Score 369.5; DB 2; Length 387; 35.0%; Pred. No. 9.4e-27; tive 45; Mismatches 102; Indels 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTONCEVYRSVDLAFFITLSFTYMNSMLDPVVYYFSSPSF 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                246 --NACALLETIRRALYITSKLSDANCCLDAICYYYMAKEF 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                         A, Gene: HM74
C, Superfamily: G protein-coupled receptor 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           66 FVFTLPPRIFYF-TTRNWPPGDLLCKISVMLFYTNWYGSILFLTCISVDRFLAIVYPFKS 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       69 LLCTLPFVLHSLRDTSDTP----LCQLSQGIYLTNRYMSISLVTAIAVDRYVAVRHPLRA 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          177 ------LIGEYLPLAVVVFCSLKVVTALAQRPPTDVGQAEATRKAKRMVWA 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               69 LLCTLPFVLHSLRDTSDTP----LCQLSQGIYLTNRYMSISLVTAIAVDRYVAVRHPLRA 124
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                                                                                                                                                                                                                                                                                                                          62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 SSNCSTEDSFKYTLYGCVFSMVFVLGLIANCVAIYIFFFTLKVRNETTTYMLNLAISDLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           222 NLLVFVVCFLPLHVGL---TVRLAVGWNACALLETIRRALYITSKLSDANCCLDAICYYY
                                                                                                                                                                                                           10 SSDLTWPPAIKLGFY-AYLGVLLVLGLLLNSLALWVFCCRMQQWTETRIYMTNLAVADLC
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                                                                                                              Gaps
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22.8%; Score 367.5; DB 2; Length 308; 30.3%; Pred. No. 1.1e-26;
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                                                                                                        64; Mismatches 102; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Superfamily: ATF receptor reu
C;Keywords: G protein-coupled receptor; transmembrane protein
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C;Accession: S68679
R;Stam, N.J.; Klomp, J.; van de Heuvel, M.; Olijve, W.
R;Stam, N.J.; Klomp, J.; van de Heuvel, M.; Olijve, W.
A;Title: Molecular cloning and characterization of a novel orphan receptor (P(2P)) expre A;Reference number: S68679; MUID:96197801; PMID:8617367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A,Residues: 1-365 <STA>
A,Residues: 1-365 <STA>
A,Cross-references: UNIPARC: UNIPARC: UPI00002E776; EMBL: X96597; NID: 91296631; PI
C;Superfamily: ATP receptor P2u
C;Reywords: G protein-coupled receptor
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                                                                                                                                                                                                                                                                                                                                                                                                           157 QEGG--FCFRSTRHNF-----NSMRFPLLGFYLPLAVVVFCSLKVVTALAORPPTDVGQ 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                          AEATRKAKRMVWANILVFVVCFLPLHVGLTVRLAVGWN-----ACALLETIRRALYITSK 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    88 ---LCQLSQGIYLTNRYMSISLVTAIAVDRYVAVRHPLRARGLRSPRQAAAVCAVLWVLV 144
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                                                                                                                                                                                                                                                                        101 YMSISLVTAIAVDRYVAVRHPLRARGLRSPRQAAAVCAVLWVLVIGSLVARWLL----GI 156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Homo sapiens (man)
C;Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
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                                    -----NTCGSSDLTWPPAIKLGF-YAYLGVLLVL----GLLLNSLALWV
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29.2%; Pred. No. 9.6e-22;
tive 56; Mismatches 123;
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Best Local Similarity 29.24
Matches 94; Conservative
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A;Status: preliminary
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ATP receptor P2u - mouse
A47556
ATP receptor P2u - mouse
C;Species: Mas musculus (house mouse)
C;Species: Mas musculus (house mouse)
C;Species: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C;Accession: A47556
E;Austig, K.D.; Shiau, A.K.; Brake, A.J.; Julius, D.
Proc. Natl. Acad. Sci. U.S.A. 90, 5113-5117, 1993
A;Accession: A47556
A;Accession: A47556
A;Accession: A7556
A;Accession: A7756
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294 TSDTIQNS 301
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Matches 96; Conserv
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bradykinin B2 receptor - human

bradykinin B2 receptor - human

c;Species: Homo sapiens (man)

c;Species: Homo sapiens (man)

c;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 09-Jul-2004

c;Accession: JH0712; A46022; Ā55559; JQ1488; JC1400

R;Eggerickx, D.; Raspe, B.; Bertrand, D.; Vassart, G.; Parmentier, M.

Biochem. Biophys. Res. Commun. 187, 1306-1313, 1992

A;Title: Molecular cloning, functional expression and pharmacological characterization of
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A;Map position: 19q13.3-19q13.3
A;Introns: #status absent
C;Superfamily: G protein-coupled receptor 4
C;Keywords: G protein-coupled receptor
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C,Superfamily: ATP receptor P2u
C;Keywords: G protein-coupled receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A Molecule Lype: DNA
A)Residues: 1-354 «RES»
A)Residues: 1-354 «RES»
A)Residues: 1-354 «RES»
C)Superfamily: G protein-coupled receptor 4
C)Superfamily: G protein-coupled receptor 5
C)Keywords: G protein-coupled receptor
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Cispecies: Homo sapiens (man)
Cispecies: O2-U1-1996 #sequence_revision 02-U1-1996 #text_change 09-U1-2004
Cispecies: 02-U1-1996 #sequence_revision 02-U1-1996 #text_change 09-U1-2004
Cispecies: 03-U1-1996 #sequence_revision 02-U1-1996 #text_change 09-U1-2004
RiHelber, M.; Docherty, J.M.; Shah, G.; Nguyen, T.; Cheng, R.; Heng, H.H.Q.; Marchese, DNA Cell Biol. 14, 25-35, 1995
Airtie: Isolation of three novel human genes encoding G protein-coupled receptors.
A;Reference number: I53033; MUID:95134353; PMID:7832990
G protein-coupled P2 receptor - rat
G/Species: Rattus norvegicus (Norway rat)
C/Species: Rattus norvegicus (Norway rat)
C/Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C/Accession: 155450
B:Chang, K.; Hanacka, K.; Kumada, M.; Takuwa, Y.
J. Biol. Chem. 270, 26152-26158, 1995
A/Itle: Molecular cloning and functional analysis of a novel P2 nucleotide receptor.
A/Reference number: 155450; MUID:96064682; PMID:7592819
A/Accession: 155450; MUID:96064682; PMID:7592819
A/Actus: preliminary; translated from GB/EMBL/DDBJ
A/Molecule type: mRNA
A/Residues: 1-328 «RRS»
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51 QWTETRIYMTNLAVADLCLLCTLPFVLHSLRDTSDTPL----CQLSQGIYLTNRYMSISL 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VTAIAVDRYVAVRHPLRARGLRSPRQAA-AVCAVLWVLVIGSLVARWLL---GIQEG-GF 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           117 LTCISFQRYLGICHPLAPWHKRGGRRAAWVVCGVVWLVVTAQCLPTAVFAATGIQRNRTV 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CF-----RSTRHNFNSMRFPLLGFYLPLAVVVFCSLKVVTALAQR--PPTDVGQAEATR 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          214 KAKRMVWANLLVFVVCFLPLHVGLTVRLAVGWN---ACALLETIRRALYITSKLSDANCC 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MINLAVADLCLLCTLP----FVLHSLRDTSDTPLCQLSQGIYLTNRYMSISLVTAIAVDR 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 NGTY-----NTCGSSD----LTWPPAIKLGFYAYLGVLLVLGLLLNSLALWVFCCRMQ 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28
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19.3%; Score 311.5; DB 2; Length 354;
Best Local Similarity 31.3%; Pred. No. 2.2e-21;
Matches 94; Conservative 48; Mismatches 117; Indels 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19.4%; Score 314; DB 2; Length 328; 30.3%; Pred. No. 1.2e-21; ive 48; Mismatches 131; Indels
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LDPILFYFTQQKFR 309
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Best Local Similarity 30.3*
Matches 95; Conservative
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A, Accession: A41283
A, Molecule type: mRNA
A, Residues: 1-36 <MCE>
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A;Molecule type: DNA
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A;Residues: 10;R.; Sources: University G.S.; Strader, C.D.; Ransom, R.W.
Biochem. Biophys. Res. Commun. 184, 260-268, 1992
Biochem. Biophys. Res. Commun. 184, 260-268, 1992
A;Title: Cloning and pharmacological characterization of a human bradykinin (BK-2) reception: Joi488; MUID:92231936; PMID:1314587
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A;Residues: 1-364 «HES>
A;Cross-references: UNIPARC:UPI00002A4FC; GB:M88714; NID:g1387999; PIDN:AAB02793.1; PID
   A;Reference number: JH0712; MUD:93038601; PMID:1329734
A;Accession: JH0712
A;Accession: JH0722
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R;Ma, J:; Wang, D.; Ward, D.C.; Chen, L.; Dessai, T.; Chao, J.; Chao, L.
Genomics 23, 352-369, 1994
A;Title: Structure and chromosomal localization of the gene (BDKRB2) encoding human } A;Reference number: A55559; MUID:95137582; PMID:7835885
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    123 LVSIDRYLALVKTWSMGRWRGVRWAKLYSLVIWGCTLLLSSPMLVFRTMKEYSDEG---- 178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EATRKAKRMVWANLLVFVVCFLPLHVGLTV----RLAVGWNACALLETIRRALYITSKLS 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : |:| :| ||:|::|:|| :: | |: : || : :| | |: :| | |: :| | |: :| | |: :| | |: :| | |: :| | |: :| | |: :| |: :| | |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MNGTYNTCGSSDLTW-----PPAIKLGFYAYLGVLLVLGLLLNSLALWVFCCRMQQW
Reference number: JH0712; MUID:93038601; PMID:1329734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRHN----
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A,Molecule type: DNA
A,Residues: 1-364 <POW>
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bradykinin receptor type B-2 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 09-Jul-2004
C;Accession: A41283, A55079; 547529
R;McBachern, A.E.; Shelton, E.R.; Bhakta, S.; Obernolte, R.; Bach, C.; Zuppan, P.; Fujis Proc. Natl. Acad. Sci. US.A. 88, 7724-7728, 1991
A;Title: Expression cloning of a rat B-2 bradykinin receptor.
A;Reference number: A41283; MUID:91352062; PMID:1715575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Conserved to MINTROT: P25023; UNIPARC: UPI00001708A1; GB: M59967
A; Cross-references: UNIPROT: P25023; UNIPARC: UPI00001708A1; GB. M59967
B; Pesquero, J.B.; Lindsey, C.J.; Zeh, K.; Paiva, A.C.M.; Ganten, D.; Bader, M.
J. Biol. Chem. 269, 26920-26925; 1994
A; Title: Molecular structure and expression of rat bradykinin B2 receptor gene. Evidence A; Reference number: A55079; MUID: 95014558; PMID: 7929432
A; Accession: A55079
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C; Superfamily: vertebrate rhodopsin
C; Superfamily: vertebrate rhodopsin
F; Stewords: alternative splicing; G protein-coupled receptor; glycoprotein; lipoprotein, F; 31-48/Domain: transmembrane #status predicted <TM1>
F; 79-96/Domain: transmembrane #status predicted <TM4>
F; 154-170/Domain: transmembrane #status predicted <TM4>
F; 197-215/Domain: transmembrane #status predicted <TM5>
F; 197-215/Domain: transmembrane #status predicted <TM5>
F; 197-215/Domain: transmembrane #status predicted <TM5>
F; 255-261/Domain: transmembrane #status pre
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A;Residues: 1-75,44,77-366 <PES>
A;Residues: 1-75,44,77-366 <PES>
A;Cross-references: UNIPARC:UP1000002A4FE; GB:X80187; GB:X80188; GB:X80189; GB:X80190
R;Wang, D.; Ma, J.; Chao, L.; Chao, J.
Biochim: Biochim: Biochim; Biochim; Biochim; Biochim; Biochim; Biochim; Biochim; Cloning and sequence analysis of rat bradykinin B(2) receptor gene.
A;Title: Molecular cloning and sequence analysis of rat bradykinin B(2) receptor gene.
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295 YSNSCLNPLVYVIVGKRFRKKS 316
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completed: February 9, 2006, 01:01:14
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Best Local Similarity
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A; Status: preliminary
A; Molecule type: mRNA
A; Molecule: 1-342 < HON>
A; Cross-references: UNIPROT: P21556; UNIPARC: UPI00001311EE; GB: X56736; NID: 949442; PIDN: C
A; Note: the species of guinea pig is not identified; in GenBank entry CCPAFREC, release
C; Superfamily: ATP receptor P2u
                                                                                                                                                                                                                 C;Species: Cavia porcellus (guinea pig)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C;Accession: S13538
R;Honda, Z.; Nakamura, M.; Miki, I.; Minami, M.; Watanabe, T.; Seyama, Y.; Okado, H.; To Nature 349, 342-346, 1991
A;Title: Cloning by functional expression of platelet-activating factor receptor from gu A;Reference number: S13638; MUID:91101726; PMID:1846231
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B15761

B15761

G protein-coupled receptor 4 - pig

G protein-coupled receptor 4 - pig

C;Species: Sus scrofa domestica (domestic pig)

C;Date: 08-Feb-1996 #sequence_revision 08-Feb-1996 #text_change 09-Jul-2004

C;Accession: B57641

R;Mahadevan, M.S.; Baird, S.; Bailly, J.E.; Shutler, G.G.; Sabourin, L.A.; Tsilfidis, C.Genomics 30, 84-88, 1995

A;Title: Isolation of a novel G protein-coupled receptor (GPR4) localized to chromosome A;Reference number: A57641; MUID:96129306; PMID:8595909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A/Status: preliminary; nucleic acid sequence not shown; translation not shown; significs
A/Molecule type: DNA
A/Residues: 1-362 <MAH>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  186 VVVPCSLKVVTALAQRPPTDVGQAEATRKAKRMVWANLLVFVVCFLPLHVGLTVRLAVGW 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  201 LILFCNLVIIHTLIRQPVKQQRNAEVRRRALMMVCTVLAVFVICFVFHHM-----VQLPW 255
247 VLAVLGLFVLCWFPFQISTFLDTLLRLGVLSGCWN------ERAVDIVTQISSYVAYS 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24 IIFVLGIIANGYVLWVP-ARLYPSKKLNBIKIFWVNLTVADLLPLITLPLMIVYSYSNQGN 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                84 SDTP--LCQLSQGIYLTNRYMSISLVTAIAVDRYVAVRHPLRARGLRSPRQAAAVCAVLW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29 VLLVIGLLINSLALMVFCCRM---QCWTETRIYMTNLAVADICLLCTLP--FVLHSLRDT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                246 NACAL-----LETIRRALYITSKLSDANCCLDAICYYYMAKEFQE 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19.1%; Score 309; DB 2; Length 342; 28.2%; Pred. No. 3.6e-21; ive 58; Mismatches 110; Indels
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19.1%; Score 308.5; DB 2;
Best Local Similarity 30.6%; Pred. No. 4.3e-21;
Matches 93; Conservative 48; Mismatches 114;
                                                                                                                                                                                               platelet-activating factor receptor - guinea pig
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C;Superfamily: G protein-coupled receptor 4
C;Keywords: G protein-coupled receptor
                                                                                    299 NSCLNPLVYVIVGKRFRKKS 318
                                         268 NCCLDAICYYYMAKEPQEAS 287
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Best Local Similarity 28.2<sup>3</sup>
Matches 81, Conservative
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RESULT 15
S06207
G protein-coupled receptor 6C.1 - human
C;Species: Homo sapiens (man)
C;Date: 15-Peb-1997 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C;Date: 15-Peb-1997 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C;Date: 15-Reb-1997 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C;Accession: $68207
R;Ah, S.; Tasi, C.; Goetzl, E.J.
FEBS Lett. 312-1124, 1995
A;Title: Cloning, sequencing and tissue distribution of two related G protein-coupled rec
A;Accession: $68207
A;Cossion: $68207
A;Accession: $68207
A;Ac
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         174 RFPL-------LGFYLPLAVVVFCSLKVVTALAQRPPTDVGQAEATRKAKRMVW 220
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                                                         3 NGTWEGCHVDSRVDHLFPPSL-----YIFVIGV-GLPTNCLRLWAAYRQVRQRNELGVY
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171 KPPMBGWVAWMNLYRVFVGFLFPWALMLLSYRGILRAVRGSVST---BRQEKAKIKRLAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  217 RMVWANILLVFVVÇPLPLHVGLTVRLAV----GWNACALLETIRRALYITSKLSDANCCLD
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NGTYNTC---GSSDLTWPPAIKLGFYAYLGVLLVLGLLLNSLALWVFCCRMQQWTETRIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 NGTYNTC---GSSDLTWPPAIKLGFYAYLGVLLVLGLLLNSLALWVFCCRMQQWTETRIY
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                                                                                                                                                                                                 59 MTNLAVADLCLLCT
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homo sapien homo sapien xenopus lae homo sapien sus scrofa

048pq4 080239 080239 080239 080232 P41232 P41231 065xg86 095xg86 069852 069852 086131 045x91 045x91 069852

mus musculu

rattus norv

xenopus tro rattus norv homo sapien

mus musculu

sus scrofa

309 AA

protein

Run on:

Sequence:

Searched:

Database

Result

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RA Halleck A., Ebert L., Mkoundinya M., Schick M., Eisenstein S.,
Rah Halleck A., Ebert L., Mkoundinya M., Schick M., Eisenstein S.,
Rubert P., Katrang K., Schatten R., Shen B., Henze S., Mar W.,
Rah Korn B., Zuo D., Hu Y., LaBaar J.;
Esubmitted (JUN-2004) to the EMBL/GenBank/DBBJ databases.
C. -: SUBCELJULAR LOCATION: Integral membrane protein (By similarity).
C. -: SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
DR EMBL, CRSJIFS; CAGA6564.1; -: MRNA.
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:001616; P:rhodopsin-like receptor activity; IEA.
DR GO; GO:00154; F:rhodopsin-like receptor protein signalin. .; IEA.
DR FAMPS; PRO001; 7fm 1; 1.
DR PROSITE; PSC0237; GPCRRHODOPSN.
PROSITE; PSC0237; GPROTEIN RECEP_FI_1; 1.
PROSITE; PSC0223; GPROTEIN RECEP_FI_2; 1.
ROSITE; PSC0224; GPROTEIN RECEP_FI_2; 1.
ROSITE; PSC0262; GPROTEIN RECEP_FI_2; 1.
ROSITE; PSC0263; GPROTEIN RECEP_FI_2; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
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Pred. No. 7.1e-112;
0; Mismatches 2;
                080239_RAT
08VES4_MOUSE
PERYZ_HUMAN
04VBNI_HUMAN
05KGS6_XENLA
CPR81_HUMAN
CLIRE_PIG
06P852_XENTR
GPR81_MOUSE
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                                                                                                                                                                                                                                    RAT
7 HUMAN
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Matches 307; Conservative
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05-JUL-2004 (TrEMBLrel.
05-JUL-2004 (TrEMBLrel.
[1] _
NUCLEOTIDE SEQUENCE.
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NCBI_TaxID=9606;
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Name=GPR35;
341
337.5
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Q47EY2 HUMAN

Q47EH2 HUMAN

Q87EX12 HUMAN

Q8CES MOUSE

Q8CES MOUSE

Q8ES B MOUSE

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Q8ES F HUMAN

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LAVGWNACALLETIRRALYITSKLSDANCCLDAICYYYMAKRPQEASALAVAPRAKAHKS 300
                   241 LAVGWNACALLETIRRALYITSKLSDANCCLDAICYYYWAKEFQEASALAVAPRAKAHKS 300
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910, G0:0005887; C:integral to plasma membrane; TAS.

G0; G0:0005887; F:G-protein coupled receptor activity; TAS.

G0; G0:0007186; F:G-protein coupled receptor protein signalin. . .; TAS.

InterPro; IPR000276; GPCR_Rhodpsn.
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MEDLINE-20472315; PubMed=11017071; DOI=10.1038/79876;

Horikawa Y., Oda N., Cox N.J., Li X., Orho-Melander M., Hara M., Hincklo Y., Lindner T.H., Mashima H., Schwarz P.E.H., Gostoe-Plata L., Horikawa Y., Oda Y., Yoshiuchi I., Colilla S., Polonsky K.S., Wei S., Concannon P., Iwasaki N., Schulze J., Baier L.J., Bogardus C., Groop L., Boerwinkle E., Hanis C.L.,
                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'Genetic variation in the gene encoding calpain-10 is associated with type 2 diabetes mellitus."; The Genet. 26:163-175(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
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NUCLECTIDE SEQUENCE, AND VARIANT ARG-294.

MUCLINE=98140132; PubMed=9479505; DOI=10.1006/geno.1998.5095;

O' Dowd B.P., Nguyen T., Marcheee A., Cheng R., Lynch K.R.,
Heng H.H.Q., Kolakowski L.P. Jr., George S.R.;

"Discovery of three novel G-protein-coupled receptor genes.";
                                                                                                                       GPR35 HUMAN STANDARD,

AC QHC97, 043495, Q86H4,

AT 16-OCT-2001 (Rel. 40, Created)

DT 13-SEP-2005 (Rel. 48, Last sequence update)

DT 13-SEP-2005 (Rel. 48, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF027957; AAC52028.1; -; Genomic_DNA.
EMBL; AF089097; AAG17965.1; -; mRNA.
EMBL; AZ75467; AAP32299.1; -; Genomic_DNA.
Ensembl; ENSG00000178623; Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA]
                                                                                                                                                                                                                                                                                                                                                                           Genomics 47:310-313(1998).
                                                   ODSLCVTLA 309
                                                                   ODSLCVTLA 309
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Pfam, PF00001; 7tm 1; 1.

PROMING, PRO0237; GFCRRHDODEN.

PROSITE; PS00237; G PROTEIN RECEP F1 1; 1.

PROSITE; PS50262; G-PROTEIN_RECEP_F1_2; 1.

PROSITE; PS50262; G-PROTEIN_RECEP_F1_2; 1.

Transducin coupled receptor; Glycoprotein; Polymorphism; Receptor; Transmembrane.

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Cytoplasmic (Potential).
N-linked (GlcNAc. . .) (Potential).
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Cytoplasmic (Potential).
2 (Potential).
Extracellular (Potential)
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Cytoplasmic (Potential).
6 (Potential).
Extracellular (Potential)
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/FTId=VAR_013606.
A -> R (in Ref. 1).
97734FB7231B26F0 CRC64;
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99.0%;
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Q4ZFV2;
13-SEP-2005 (TrEMBLrel. 31,
13-SEP-2005 (TrEMBLrel. 31,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 306; Conservative
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309 AA;
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Kawakami B., Sugiyama A., Takemoto M., Sugiyama T., Irie R.,
Kawakami B., Sugiyama A., Takemoto M., Sugiyama T., Irie R.,
Cawakami B., Sato H., Ota T., Wakamatsu A., Ishii S., Yamamoto J.,
Ra Isono Y., Kawai-Hio Y., Saito K., Nishikawa T., Kimura K.,
Ra Yamashita H., Matsuo K., Nakamura Y., Sekine M., Kikuchi H.,
Ra Yamashita H., Murakawa K., Kanehori K., Takahashi-Fujii A., Oshima A.,
Ra Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.;
Submitted (MAR-2004) to Che EMBL/GenBank/DDBJ databases.
C. -- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
REML, AK131540; BAD18676.1; -; mRNA.
REML, AK131540; BAD18676.1; -; mRNA.
RO; GO:00017842; Fricceptor activity: IEA.
GO; GO:0001844; Fricceptor activity: IEA.
GO; GO:0001849; Fricocoptor activity: IEA.
GO; GO:0001849; Fricocoptor activity: IEA.
RO; GO:0007186; Pricocoptor activity: IEA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 receptor protein signalin. . ., IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 PLRARGLRSPRQAAAVCAVLWVLVIGSLVARWLLGIQEGGFCFRSTRHNFNSMRFPLLGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                266 YLPLAVVVFCSLKVVTALAQRPPTDVGQAEATRKAARMWANLLVFVVCFLPLHVGLTVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 NLAVADLCLLCTLPFVLHSLRDTSDTPLCQLSQGIYLTNRYMSISLVTAIAVDRYVAVRH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     206 PLRARGIRSPRQAAAVCAVLWVLVIGSLVARWLLGIQEGGFCFRSTRHNFNSWAFPLLGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YLPLAVVVFCSLKVVTALAQRPPTDVGQAEATRKAKRMVWANLLVFVVCFLPLHVGLTVR
                                                  Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MNGTYNTCGSSDLTWPPAIKLGFYAYLGVLLVLGLLLNSLALWVFCCRMQQWTETRIYMT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PERMY PROGOT, 7tm 1, 1.

PRINTS; PRO0237; GPCRRHODOPSN.

PRINTS; PRO0237; GPRRHODOPSN.

PROSITE; PSO0262; GPROTEIN RECEP F1_1; 1.

G-protein coupled receptor; Receptor; Transmembrane.

SEQUENCE 394 AA; 43309 MW; 1598FD44BAR4233C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 98.9%; Score 1597; DB 2; Best Local Similarity 99.0%; Pred. No. 2.5e-111; Matches 306; Conservative 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            308 AA.
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Hypothetical protein FLJ16773.
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13-SEP-2005 (TrEMBLrel. 31,
13-SEP-2005 (TrEMBLrel. 31,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q4VBN5_HUMAN PRELIMINARY;
Q4VBN5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GPR35 protein (Fragment).
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                                                                                                                                                   NCBI_TaxID=9606;
                                                                                                                                                                                                                                           TISSUE=Brain;
                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name=GPR35;
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      SOOCC CCC RAPARTER RANGO CCC CCC RAPARTER RANGO CCC CCC RAPARTER R
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MNGTYNTCGSSDLTWPPAIKLGFYAYLGVLLVLGLLLNSLALWVFCCRMQQWTETRIYMT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MNGTYNTGGSSDLTWPPAIKLGFYAYLGVLLVLGLLLNSLALWVFCGRWQQWTBTRIYMT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (ARR-2005) to the EMBL/GenBank/DDBJ databases.

1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).

1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.

EMBL; AC124862; AAX88945.1; -; Genomic_DNA.

InterPro; IRR000276; GFR Rhodpsn.

Pfam; PF00001; 7tm 1; 1.

PRINTS; PR00237; GFRCRHODDPSN.

PROSITE; PS00237; GFRCRHODDPSN.

G-protein coupled receptor; Hypothetical protein; Receptor;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98.9%; Score 1597; DB 2; Length 309; 99.0%; Pred. No. 2e-111; ive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                    Haakenson W., Trani L., Schatzkamer K.; "The sequence of Homo sapiens BAC clone RP11-27M15."; Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Waterston R.H.;
Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              309 AA; 34072 MW; 97734FB7231B26F0 CRC64;
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Last annotation update)
      Last annotation update)
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                               Hypothetical protein GPR35
Name=GPR35;
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QEZMP9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Transmembrane
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         13-SEP-2005 (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Waterston R.;
Submitted (OCT-2002)
                                                                                              Homo sapiens (Human)
                                                                                                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUCLEOTIDE SEQUENCE
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                                                                                                                                                                                                                  NCBI_TaxID=9606;
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05-JUL-2004
05-JUL-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wilson R.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Transducer;
SEQUENCE 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19
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Length 394; Indela 145 120 205 180

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TISSUB—G-protein coupled receptors;

NEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RETARREPERS R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Altachul S.F., Zeeberg B.B., Wagner L., Shemmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B.B., Burder T., Max S.I., Wang J., Haieh F.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,

Batchenko L., Marusina K.R., Farmer A.A., Rubin G.M., Hong L.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abrameon R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Nilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Schnerch A., Schein J.B., Jones S.J.M., Marra M.A.,

"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 LPLAVVVFCSLKVVTALAQRPPTDVGQARATRKAARMVMANILVFVVCFLPLHVGLTVRL 240
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Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NGTYNTCGSSDLTWPPAIKLGFYAYLGVLLVLGLLLNSLALWVFCCRMQQWTETRIYMTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
EMBL: BC095500; AAH95500.1; -; mRNA.
InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm 1; 1.
PRINTS; PF00237; GPCRHODOPSN.
PROSITE; P600237; GPCRHODOPSN.
PROSITE; P600237; GPCRHODOPSN.
G-protein coupled receptor; Receptor; Transmembrane.
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308 AA; 33941 MW; 5791BF9CB7206034 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUB=G-protein coupled receptors; NIH MGC Project;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cDNA sequences
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                                    NCBI TaxID=9606;
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SEQUENCE
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MEDINE-2788-25; PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDINE-2788-25; PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDINE-2788-25; PubMed=12477932; DOI=10.1073/pnas.242603899;

MIAUSDER R.D., Colling F.S., Wagger L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A platchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A platchenko L., Marusina K., Parmer A.A., Rubin G.M., Scheetz T.E.,

Brownstein M.J. Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Millahy S.J.,

Bosak S.A., McKernan K.J., Malek J.A., Gunzatne P.H.,

Rahas S.S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Radriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

B. Mark B. J. J. J. Length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EWBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
                                                                                                                                                           Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Genetic variation in the gene encoding calpain-10 is associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WUCLEOTIDE SEQUENCE.

MEDLINE=20472315; PubMed=11017071; DOI=10.1038/79876;

HORIKAWA Y., Oda N., COX N.J., Li X., Orho-Melander M., Hara M.,

Hinokio Y., Lindher T.H., Mashima H., Schwarz P.E.H.,

del Bosque-Plata L., Horikawa Y., Oda Y., Yoshiuchi I.,

Polonsky K.S., Wei S., Concannon P., Iwasaki N., Schulze J.,

Baier L.J., Bogardus C., Groop L., Boerwinkle E., Hanis C.L.,
                                       16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Probable G-protein coupled receptor 35.
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EMBL; BCC27429; AAH77429.1; -; mRNA.
ENSembl; ENSWUSG000002521; Mus musculus.
MGI; MGI:1929509; Gpr35.
GO; GO:0016021; C:Intregral to membrane; TAS.
InterPro; IPR002286; GPCR, Rhodpsn.
InterPro; IPR002286; P2_Durnocptor.
    307 AA
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PRINTS; PR00237; GFCRRHODOPSN.

PRINTS; PR01157; P2YPURNOCPTR.

PROSITE; PS00237; G PROTEIN RECEP F1 1; 1.

PROSITE; PS50262; G PROTEIN RECEP F1 2; 1.
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t. Genet. 26:163-175(2000).
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    STANDARD;
                                                                                                                                                Mus musculus (Mouse)
                                                                                                                                                                                                                                      NCBI_TaxID=10090;
GPR35 MOUSE
Q9ES90;
                                                                                                                               Name=Gpr35;
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Query Match
Best Local Simi:
Matches 223;
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                                                                                                                                                                                                                                                                                                      HPLRARGLRSPRQAAAVCAVLWVLVIGSLVARWLLGIQEGGFCFRS-TRHNFNSMRFPLL 178
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini, Hominidae,
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"Probable G-protein coupled receptor.";
Submitted (ARR-2000) to the EMBL/GenBank/DDBJ databases
--- SUBCELLULAR LOCATION: Integral membrane protein (By similarity)
--- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
EMBL; AB041940; BADB3594.1; -; mRNA.
                                                                                                                                         Cytoplasmic (Potential).
N-linked (GlcNAc. . ) (Potential).
N-linked (GlcNAc. . . ) (Potential).
By similarity.
Glycoprotein; Receptor; Transducer;
                                                                                                                                                                                                                 ;
6
                                                                                                                                                                                             Length 307;
                                                                                                                                                                                                                51; Indels
                                  Cytoplasmic (Potential).
2 (Potential).
Extracellular (Potential).
                                                                             4 (Potential).
Extracellular (Potential).
                                                                                                              6 (Potential).
Extracellular (Potential)
7 (Potential).
                                                                                                                                                                             0B3D02CECB16710D CRC64;
                  Extracellular (Potential)
                                                            3 (Potential).
Cytoplasmic (Potential).
                                                                                               5 (Potential).
Cytoplasmic (Potential).
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Last annotation update)
                                                                                                                                                                                             ;; Score 1123; DB 1;
;; Pred. No. 5.3e-76;
30; Mismatches 51;
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                                                                                                                                                                              34152 MW;
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  receptor;
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Name=KPG 007;
Homo sapiens (Human).
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QSKU21;
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hes 223; Conservative
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KSQDSQILSL 306
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307 AA;
 G-protein coupled
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          Fransmembrane
ropo DOM
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=CS7BL/65; TISSUE-Bone; MEDLINE-99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9; Carminci P., Hayashizaki Y.; "High-efficiency full-length cDNA cloning."; Meth. Enzymol. 303:19-44(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MNGTYNTCGSSDLTWPPAIKLGFYAYLGVLLVLGLLLNSLALWVFCCRMQQWTFTRIYMT
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Glires, Rodentia, Sciurognathi,
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MEDLINE-21085660; PubMed-11217851; DOI-10.1038/35055500;
Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
                                                                                                                                                                                                                      Pfam, PF00001; 7tm 1; 1.
PRINTS, PRODATI, GPCRRHDODEN.
PRINTS; PRO1157; PZYPURNCCPTR.
PROSITE; PS00237; G_PROTEIN RECEP_F1_1; 1.
PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled G_ECEPTORIN_RECEP_F1_2; 1.
G-protein coupled A; 34152 MW; 0B3D02CECB16710D CRC64;
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GO, GO:0016021, C:integral to membrane; IEA.
GO; GO:0045028; F:purinergic mucleotide receptor activity, G-.
GO; GO:0004872; F:receptor activity; IEA.
GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
GO; GO:0007186; F:G-protein coupled receptor protein signalin.
GO; GO:0007186; P:g-protein coupled receptor protein signalin.
InterPro; IPR000276; GPCR. Rhodops.
InterPro; IPR002286; P2_purnocptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                             69.5%; Score 1123; DB 2; Length 3
71.9%; Pred. No. 5.3e-76;
ive 30; Mismatches 51; Indels
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Mus musculus adult male bone cDNA, RIKEN full-length enz
clone:9830121M19 product:G protein-coupled receptor 35,
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Q8CB97;
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A Arawaw T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Gojobori T., Bono H., Ksaikwa T., Saito R., A Kadote K., Matsuda H.A., Ashburnar M., Batalov S., Casavant T., Rieschmann W., Gasterland T., Gissi C., King B., Kochiwa H., A Kubhl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Schriml L.M., Staubli F., Suzuki R., Tomita M., Magner L., Washio T., Bakai K., Okido T., Puruno M., Aono H., Baldarelli R., Barsh G., Brownstein M.J., Bult C., Fletcher C., Fullia M., Gariboldi M.F., Brownstein M.J., Boffelli D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchlonni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., A Sasaki H., Sato K., Schophach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Manshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=C57BL/6J; TISSUE=Bone;
The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=C57BL/6J; TISSUE=Bone;
MEDILIRE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
MEDILIRE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
Mormalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                      "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
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GO; GO:0016021; C:Integral to membrane; TAS.
InterPro; IPR000276; GPCR Rhodpsn.
InterPro; IPR002286; P2_purnocptor.
Pfam; PP00001; 7tm_1; 1.
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TISSUE=Smbryonic body between diaphragm region and neck;

MEDLINE-21005660; PubMed=11217851; DOJ=10.1038/35055500;

Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

Arakawa T., Hara A., Fukunishii Y., Konno H., Adachii J., Fukuda S.,

Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

Salto T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,

Fleischmann W., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
                                                                                                                                                                                                                                                                   1 MNGTYNTCGSSDLTWPPAIKLGFYAYLGVLLVLGLLLNSLALWVFCCRMQQWTETRIYMT
                                                                                                                                                                                                                                                                                            GFYLPLAVVVFCSLKVVTALAQRPPTDVGQABATRKAKRMVWANLLVFVVCFLPLHVGLT
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
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TISSUE=Embryonic body between diaphragm region and neck;
MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QERSOB MOUSE PRELIMINARY; PRT; 307 AA.
(281599)
10-MAR-2003 (TrEMBLrel. 23, Created)
10-MAR-2003 (TrEMBLrel. 23, Last sequence update)
10-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Mus musculus 12 days embryo embryonic body between diaphragm region and nack cDNA, RIKEN full-length enriched library, clone:9430051L15 product:G protein-coupled receptor 35, full insert sequence.
                                                                                                    Transducer; Transmembrane,
                                                                                                                                                                                                                        . 9
                                                                                                                                                                      Query Match 69.5%; Score 1122; DB 2; Length 307; Best Local Similarity 71.9%; Pred. No. 6.2e-76; Matches 223; Conservative 30; Mismatches 51; Indels
PRINTS; PR00237; GPCRRHODOPSN.
PRINTS; PR01157; P2YPURNOCPTR.
PROSITE; PS00237; G PROTEIN RECEP F1 1; 1.
PROSITE; PS0262; G PROTEIN RECEP F1 2; 1.
G-protein coupled recepcor; Receptor; Transducer; Trans SEQUENCE 307 AA; 34140 MM; 8EB439AAED5F7656 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Carninci P., Hayashizaki Y.; "High-efficiency full-length cDNA cloning."; Meth. Enzymol. 303:19-44(1999).
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TISSUB-Embryonic body between diaphragm region and neck;
TISSUB-Embryonic body between diaphragm region and neck;
Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
Adachi J., Aizawa K., Akimura T., Haraka T., Harozane T.,
Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
A Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kaukawa T.,
Karoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakauwa T.,
Nishi K., Nomura K., Numazaki R., Ohno M., Ohato N., Okazaki Y.,
A salto R., Saltoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanka T.,
Tomaru A., Toya T., Yasunishi A., Muramaten M., Hayashizaki Y.;
Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
Submitted (JUL-2011) to the EMBL/GenBank/DBJ databases.
Submitted (JUL-2011) to the EMBL/GenBank/DBJ databases.
Submitted (JUL-2011) to the EMBL Gental membrane protein (By similarity).
Submitted (JUL-2011) to the EMBL Gental membrane protein (By similarity).
Submitted (JUL-2011) to the EMBL Gental membrane protein (By similarity).
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C TISSUB=Embryonic body between diaphragm region and neck;

TISSUB=Embryonic body between diaphragm region and neck;

REDINES-20530913; PubMed=11076861; DOI=10.1101/gr.152600;

Shibata K., Itoh M., Alzawa K., Nagaoka S., Sasaki N., Carninci P.,

Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,

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Rujiwake S., Inoue K., Togawa Y., Izawa M., Ohara B., Watshiki M.,

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"RIKEN integrated sequence analysis (RISA) system-384-format

Genome Res. 10:1757-1771(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUB-Embryonic body between diaphragm region and neck;
MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizari Y.,
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000).
Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodziyuez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyo-Oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Wynshaw Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                               the RIKEN Genome Exploration Research Group Phase I & II Team; "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."; Nature 420:563-573 (2002).
                                                                                                                                                                                                                                                                   "Functional annotation of a full-length mouse cDNA collection.";
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TISSUE=Embryonic body between diaphragm region and neck;
The PANTOM Consortium,
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PRINTS; PR01157; P2YPURNOCPTR.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
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GO; GO:0016021; C:integral to membrane;
InterPro; IPR000276; GPCR_Rhodpsn.
InterPro; IPR002286; P2_purnocptor.
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-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is preliminary data.
-!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
                                                                                                                      Gaps
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13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
Chromosome I CAF7335, whole genome shotgun sequence. (Fragment).
ORFNames=GSTENG00004207001,
Tetraodon nigroviridis (Green puffer).
Tetraodon nigroviridis (Green puffer)
Actinopterygii, Neopterygii, Teleostei, Buteleostomi;
Actinopterygii, Neopterygii, Percomorpha, Tetraodontiformes;
Tetradontoidea, Tetraodontidae, Tetraodon.
                 Transmembrane.
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9
                                                                         tch 68.6%; Score 1108; DB 2; Length 307; al Similarity 71.3%; Pred. No. 6.9e-75; 221; Conservative 30; Mismatches 53; Indels
                 G-protein coupled receptor; Receptor; Transducer; Tran SEQUENCE 307 Aa; 34260 MW; 923D02CECB0D70AC CRC64;
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PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
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Nature 431:946-957(2004).
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                                                                                    Query Match
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                                                                                                                          Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 :|| : |||| | ::| :| | | ::| | | ::| | | ::| | | ::| | :| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           122 LRARGLRSPRQAAAVCAVLWVLVIGSLVARWLLGIQEGGF------CF----RST 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       224 LVFVVCFLPLHVGLTVRLAVGWNACAL--LETIRRALY-ITSKLSDANCCLDAICYYYMA 280
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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

A Klausher R.D., Collins P.S., Wagner L.H., Derge J.G.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haleh F.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Diatchenko L., Marusina K., Permer A.A., Rubin G.M., Hong L.,

A Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S. Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Villalon D.K., Muzny D.M., Sodergern E.J., Lu X., Gibbs R.A.,

Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7 NETGMEDCGIDDSFKYNLYSVVYSVVFVLGLITNCAALFVFCFRMKMRNETTMFMTNLAL 66
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      167 RHNFNS---MRPPLLGFYLPLAVVVFCSLKVVTALAQRPPTDVGQAEATRKAKRMVWANL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   239 GIFIICEVDENSILFLYALVRIQALASCGVERPARTLYPITLCLATLNCCLDDVVYYFTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6 NTCGSSDLTWPPAIKLGFYAYL-GVLLVLGLLLNSLALWVFCCRMQOWTETRIYMTNLAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
-i- SIMILARITY: Belongs to the G-protein coupled receptor 1 family. Bablic, CARSO112.1, -i, Genomic_DNA. InterPro, IPR000276; GPGR, Rhodpsn. InterPro, IPR00216; GPGR, Rhodpsn. InterPro, IPR002188; P2Y5_purnocptor.
                                                                                                                                 Pfam; PF00001; 7tm 1; 1.

PRINTS; PR00237; GPCRRHODOPSN.

PRINTS; PR01067; PZYSORPHARR.

PROSITE; PS00237; G PROTEIN RECEP F1 1; 1.

PROSITE; PS50262; G PROTEIN RECEP F1 2; 1.

G-protein coupled receptor; Receptor; Transducer; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         25.8%; Score 416.5; DB 2; Length 305; 34.6%; Pred. No. 3.3e-23; Artive 59; Mismatches 108; Indels 33
                                                                                                                                                                                                                                                                                                                                                                                        305 AA; 34283 MW; E9F740AD3FF04F32 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 106; Conservative
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Q502U9;
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NUCLEOTIDE SEQUENCE.
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299 ESFQKS 304
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13-SEP-2005
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104 WPPGDT-LCKISGTAPLTNIYGSMLPLTCISVDRFLAIVYPFRSRIIFTRRNSAIVCAGV 162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        44 AVSVVFILGLITNSVSLFVFCFRMKMRSETAIFITNLAVSDLLFVCTLFFKIFYNFNRH 103
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Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota, Metazoa, Chordata; Craniata, Vertebrata, Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25 AYLGVLLVLGLLLNSLALWVPCCRMQQWTETRIYMTNLAVADLCLLCTLPP-VLHSLR--
                                                                                                                                                                                                                                                                                                                                                                                                                                              1- SUBCELULAR LOCATION: Integral membrane protein (By similarity).
1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
BMBL, BC095238; AAH95538.1, -; mRNA.
BRAEML; BNSG00000147145; Home sapiens.
InterPro; IPR000276; GPCR Rhodpsn.
InterPro; IPR00218; P2Y5_purnocptor.
Pfam; PR0001, 7rm 1; 1.
PRINTS; PR00237; GPCRHODPSN.
PRINTS; PR00237; GPCRHODPSN.
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MEDLINE=97225799; PubMed=9073069; DOI=10.1016/80378-1119(96)00722-6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00237; G_PROTEIN_RECEP_F1]; 1.
PROSITE; PSS0562; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Receptor; Transducer; Transmembrane.
SEQUENCE 370 AA; 41881 MW; 38267561B1029548 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 370;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24.9%; Score 402; DB 2; Length 37: 34.1%; Pred. No. 4.7e-22; ive 60; Mismatches 111; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                   (MAY-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                           Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002)
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                                                                                                                                                                                                                                                                                                                                                TISSUE=G-protein coupled receptors;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Name=GPR23; Synonyms=P2RY9;
Homo sapiens (Human).
                                                                                                                                                                                        and mouse cDNA sequences."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 103; Conservative
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                                                                                                                                                                                                                                                                                                         NUCLEOTIDE SEQUENCE.
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Best Local Similarity
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ROUGHIES SEQUENCE LIANGE SCALE SEMENT.

ROUGH ST. Graftham D.V. Coffey A.V. Scheer S., Wolzy K., Wurny D., Ross M.T., Graftham D.V., Coffey A.V., Scheer S., Searle S., A. Landrews T.D., Scott C.E., Searle S., A. Landrews T.D., Scott C.E., Searle S., Santle S., B. Landrews T.D., Scott C.E., Searle S., Santle S., B. Landrews T.D., Scott C.E., Searle S., Santle S., B. Landrews T.D., Scott C.E., Searle S., Santle S., B. Cones M.C., Hurles M.E., Andrews T.D., Scott C.E., Searle S., Santle S., B. Cones M.C., Hurles M.E., Andrews T.D., Scott C.E., Searle S., Santle S., Santle S., Santle S., Santle S., Santle S., Market M.L., Santle S., Santle S., Market M.D., Santle S., Santle S.,
O'Dowd B.F., Nguyen T., Jung B.P., Marchese A., Cheng R., Heng H.H.Q., Kolakowski L.F. Jr., Lynch K.R., George S.R.; "Cloning and Chromosomal mapping of four putative novel human G-protein-coupled receptor genes."; Gene 187:75-81(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE.
MEDLINE=9736605; PubMed=9223435; DOI=10.1006/bbrc.1997.6895;
MAGAISNE=9736605; PubMed=9223435; DOI=10.1006/bbrc.1997.6895;
"Clanseng R., Boeynaems J.M., Godart M., Communi D.;
"Cloning of a human heptahelical receptor closely related to the P2Y5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kopatz S.A., Aronstam R.S., Sharma S.V.; "cDNA clones of human proteins involved in signal transduction sequenced by the Guthrie cDNA resource center (www.cdna.org)."; Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                          NUCLEOTIDE SEQUENCE.
Bohm S.K., Khitin L.M., Payan D.P., Bunnett N.W.;
Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Biochem. Biophys. Res. Commun. 236:106-112(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA]
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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GO:0004930; F:G-protein coupled receptor activity; TAS.
GO:0007186; P:G-protein coupled receptor protein signalin. . .; TAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        hippocampus.
                                                                                                                                                                                                                                                                                                                                                                                             Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
-1- SUBCELLULAR LOCATION: Integral membrane protein.
-1- TISSUB SPECIFICITY: Not detected in the brain regions thalamus,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PP00001; 7tm_1; 1.

PRINTS; PR00237; GPCRHODOPSN.
PRINTS; PR0167; P2YSORPHANR.
PROSITE; PS00237; G PROTEIN RECEP F1_1; 1.
PROSITE; PS50262; G PROTEIN RECEP F1_2; 1.
G-protein coupled receptor; Glycoprotein; Receptor; Transducer;
Zorilla S., Buck D., Reinhardt R., Poustka A., Rosenthal A., Lehrach H., Meindl P., Minz P.J., Hillier L.W., Willard H.F., Wilson R.K., Materston R.H., Rice C.M., Vaudin M., Coulson A. Nelson D.L., Weinstock G., Sulston J.E., Durbin R., Hubbard T Gibbs R.A., Beck S., Rogers J., Bentley D.R.; "The DNA sequence of the human X chromosome."; Nature 434:325-337(2005).
                                                                                                                                                                                                                                                                                                                                                                                                                                        putamen, caudate, frontal cortex, pons, hypothalamus and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (Potential).
Cytoplasmic (Potential).
2 (Potential).
Extracellular (Potential).
3 (Potential).
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EMBL; AY301274; AAF58404.1; -; Genomic_DNA.
EMBL; AL500083; CAD18851.1; -; Genomic_DNA.
EMBL; BC074722; AAH74722.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; U66578; AAC51301.1; -; Genomic_DNA.
EMBL; U90323; AAB62087.1; -; Genomic_DNA.
EMBL; U90322; AAB62088.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ensembl; ENSG0000147145; Homo sapiens.
HGNC; HGNC:4478; GPR23.
                                                                                                       NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR000276; GPCR_Rhodpsn.
InterPro; IPR002188; P2Y5_purnocptor.
                                                                                                                                                                                                                                                                                                                                                                                      and mouse cDNA sequences.";
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64
73
94
133
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TRANSMEM
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NUCLEOTIDE SEQUENCE.
TISSUE=PCR rescued clones;
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Matches
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
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MEDLINE-22388257; PubMed-12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.L., Wang J., Heibh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Millahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
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                                                                                                                                                                                                                                                                                                                             24.8%; Score 401; DB 1; Length 370; 34.1%; Pred. No. 5.6e-22;
                                                                                                                                                                                                                                                                                                                                                                  60; Mismatches 111; Indels
                                                       S (Potential).
Cytoplasmic (Potential).
6 (Potential).
Extracellular (Potential).
7 (Potential).
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                             4 (Potential).
Extracellular (Potential)
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N-linked (GlCNAC...) (FN-linked (GlCNAC...)
   Cytoplasmic (Potential).
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
05-JUL-2004 (TremBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                 By similarity.
P -> L (in Ref. 3)
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NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                       370 AA;
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44 AVYSVAFILGLITNSVSLFYPCFRMKMRSETAIFITNLAVSDLLFVCTLPFKIFYNFNRH 103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Director MGC Project;

Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.

-!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).

EMBL; BC069996; AAH6996:1; -; mRNA.

GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0045028; F:purithergic nucleotide receptor activity, G-. .; IEA.

GO; GO:0001884; F:rhodopsin-like receptor activity; IEA.

GO; GO:0001186; F:rhodopsin-like receptor protein signalin. .; IEA.

GO; GO:0001185; P:signal transduction; IEA.

InterPro; IRR000276; GPCR Rhodopsin-like receptor protein signalin. .; IEA.

InterPro; IRR000276; GPCR Rhodopsin-like receptor protein signalin. .; IEA.

InterPro; IRR000276; GPCR Rhodopsin-like receptor protein signalin. .; IEA.
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A., Fahey J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Schoutz A.C., Grimwood J., Schmutz D., Myers R.M., Schein J.B., Jones S.J.M., Marra M.A.; Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."
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QBEKKI;
QBEKKI;
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Mus musculus 12 days embryo spinal ganglion cDNA, RIKEN full-length
enriched library, clone:D130067B12 product:P2Y PURINOCEPTOR 9, full
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PRINTS; PR00237; GPCRRHONDEN.
PRINTS; PR010537; GPCRRHONDEN.
PROSTTE; P800237; GPROTEIN RECEP F1 1; UNKNOWN 1.
PROSTTE; P850262; G_PROTEIN RECEP F1 2; 1.
G-protein coupled receptor; Receptor; Transducer; Transmembrane.
SEQUENCE 370 AA; 41867 MW; ZAB4B3F5F43FFP83 CRC64;
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Azawa T., Hara A., Fukunishi Y., Komo H., Adachi J., Fukuda S.,
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Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
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Nasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
Whyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
Havashizaki Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the RIKEN Genome Exploration Research Group Phase I & II Team; "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
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                           Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
                                                                                                                                                                                                                                   STRAIN=C57BL/6J; TISSUE=Spinal ganglion; MEDLINE=9927953; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9; Carninci P., Hayashizaki Y.; "High-efficiency full-lengh cDNA cloning."; Meth. Enzymol. 303:19-44(1999).
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                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=C57BL/6J; TISSUE=Spinal ganglion;
MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
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The FANTOM Consortium,
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                                                                                                                    Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                227 VVCFLPLHVGLTVRLAVGWNAC--ALLETIRRALY-ITSKLSDANCCLDAICYYYMAKEF 283
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                                                                                                                                                                                                                                                                MG1; MG1:1923384; Gpr23.

GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0045028; P:purinergic nucleotide receptor activity, G-. .,; IEA.

GO; GO:0004572; F:receptor activity; IEA.

GO; GO:0001884; F:rhodopsin-like receptor activity; IEA.

GO; GO:0007186; P:G-profein coupled receptor protein signalin. .,; IEA.

GO; GO:0007186; P:signal transduction; IEA.

InterPro; IPR00276; GPCR_Rhodopsn.

InterPro; IPR002188; P2YS_purnocptor.
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259 VVCFVPYNSVLFLYALVRSQAITNCLLERFAKIMYPITLCLATLNCGFDPFIXYFTLESF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 TYNTCGSSDLTWPPAIKLGFY-AYLGVLLVLGLLLNSLALWVFCCRMQQWTETRIYMTNL
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Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Murinae; Mus.
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01-MAR-2004 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Mus musculus 9.5 days embryo parthenogenote cDNA, RIKEN full-length
enriched library, clone:Bl30055L15 product:P2Y PURINOCEPTOR 9, full
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00237; G PROTEIN RECEP_F1_1; UNKNOWN_1.
PROSITE; PS50262; G PROTEIN RECEP_F1_2; 1.
G-protein coupled receptor; Receptor; Transducer; Transmembrane.
SEQUENCE 370 AA; 41956 MW; AB126842343AE6E1 CRC64;
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24.7%; Score 399; DB 2; Length 370;
Best Local Similarity 34.3%; Pred. No. 7.9e-22;
Matches 104; Conservative 59; Mismatches 112; Indels
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PRINTS; PR01067; P2Y5ORPHANR.
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MEDLINE=21085660; PubMed=11217851; DOT=10.1038/3505500;
MARAWA J., Shinagawa A., Shibata K., Yoshino M., Itch M., Ishii Y.,
Arawawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
A Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
A Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
A Alzawa K., Isawa M., Nishi K., Kiyosawa H., Kando S., Yamanaka I.,
Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
Pleischmann W., Gasateriand T., Gissi C., King B., Kochiwa H.,
Natsudi I., M., Staubli F., Suzuki R., Tomita M., Wagner I., Washio T.,
Sakai K., Okido T., Furuno M., Anno H., Baldarelli R., Bareh G.,
Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
Blake J., Boffelli D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
Whynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
Mashhaw-Soris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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The PANTOM Consortium,
The RIKEN Genome Exploration Research Group Phase I & II Team;
The RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDMAs.";
Nature 420:563-573 (2002).
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MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
"Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libaries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000).
                                                                                                                     STRAIN=C57BL/6J; TISSUR=Parthenogenote;
MEDLINE=99279253; PLDMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
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                                          [1] TUCLEOTIDE SEQUENCE
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NUCLEOTIDE SEQUENCE
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NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                           [2]
NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               [3]
NUCLEOTIDE SEQUENCE
WCBI_TaxID=10090;
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Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.,
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
I. SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
EMBL; AKO45289; BAC32299.1; -; mRM.
EMBL; AKO45289; BAC32299.1; -; mRM.
EMBL; AKO45289; BC32299.1; -; mRM.
EMBL; AKO45289; Brithegral to membrane; IEA.

GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:00045028; F:purinergic nucleotide receptor activity, G-...; IEA.
GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
GO; GO:0001585; P:g-protein coupled receptor protein signalin. .; IEA.
GO; GO:000188; P:Prodopsin-like receptor protein signalin. .; IEA.
RO; GO:000188; P275_Purnocptor.
RITHERPO; IPRO0226; GPCR_Rhodopsn.
RITHERPO; IPRO02188; P275_Purnocptor.
RITHERPO; IRRO02188; P275_Purnocptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               104 WPFGDT-LCKISGTAFLTNIYGSMLFLTCISVDRFLALVYPFRSRTIFTRRNSALVCAGV 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  82 -DISDIPLCQLSQGIYLINRYMSISLVIAIAVDRYVAVRHPLRARGLRSPRQAAAVCAVL 140
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PRINTS; PRO1067; P2YSORPHANR.
PROSTTS; PRO1067; P2YSORPHANR.
PROSTTS; PSO50237; GENOTELN RECEP F1 1; UNKNOWN 1.
PROSTTE; PSS50262; G PROTEIN RECEP F1 2; 1.
G-protein coupled receptor; Receptor; Transducer; Transmembrane.
SEQUENCE 370 Aa; 41872 MW; 0E4C79FEDFD32050 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           249 --ALLETIRRALY-ITSKLSDANCCLDAICYYYMAKEFQEA 286
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 34.5
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Search completed: February 9, 2006, 01:00:18 Job time : 166.5 secs

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Mon Feb 13 13:14:03 2006
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Sequence 20, Appli
Sequence 159, Appli
Sequence 159, Appli
Sequence 222, Appl
Sequence 211, Appl
Sequence 21, Appli
Sequence 8, Appli
Sequence 8, Appli
Sequence 6, Appli
Sequence 10, Appli
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Sequence 10, Appli
Sequence 137, Appli
Sequence 24, Appli
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1615
1 MNGTYNTCGSSDLTWPPAIK......AVAPRAKAHKSQDSLCVTLA 309
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd
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1. /cgn2_6/ptodata/1/iaa/5_COMB.pep:*

2. /cgn2_6/ptodata/1/iaa/F_COMB.pep:*

3. /cgn2_6/ptodata/1/iaa/H_COMB.pep:*

4. /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

5. /cgn2_6/ptodata/1/iaa/RPC_COMB.pep:*

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US-10-314-048A-159
US-10-314-048A-36
US-09-170-496D-222
US-09-170-496D-222
US-09-170-496D-108
US-09-944-807-21
US-10-314-048A-135
US-08-467-948A-8
US-08-467-948A-8
US-08-467-948A-30
US-08-467-948A-30
US-08-467-948A-30
US-09-875-076-4
US-09-875-076-4
US-09-875-076-4
US-09-875-076-4
US-09-875-076-4
US-09-875-076-4
US-10-314-048A-137
US-10-314-048A-137
US-10-314-048A-137
US-09-745-842-17
US-09-745-842-17
US-09-146-88-39
US-09-146-048A-187
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US-09-585-876-2
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Listing first 45 summaries
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| 요요요리 요요리스트 바만을 만든다는다.   |              |  | 0  | 60   | 120  | 180  |
|---|--------------|--|--|--|--|--|
| 22, Appl<br>15, Appl<br>16, Appl<br>2, Appl<br>373, Ap<br>60, Appl<br>4, Appl<br>16, Appl<br>555, App<br>555, Appl<br>66, Appl<br>7, Appl<br>166, Appl<br>166, Appl<br>167, Appl<br>168, Appl<br>169, Appl<br>1  |              |  | Gaps   | FRIYMT   | FVAVRH<br>       <br>YVAVRH                                      | FPLLGF<br>   |
| Sequence   |              |  | 309;   | MOOWTE:  | AIAVDR'  | INFNSMR  |
|   |              | DIABETES   | Length 3<br>Indels                               | NNGTYNTCGSSDLTWPPAIKLGFYAYLGVLLVLGLLLNSLALWVFCCRWQOWT5TRIVMT<br> | NLAVADLCLLCTLPFVIASLRDTSDTPLCQLSQGIYLTNRYMSISLVTAIAVDRYYAVRH<br> | PLRARGLRSPRQAAAVCAVLWVLVIGSLVARWLLGIQEGGFCFRSTRHNFNSMRFPLLGF |
| 66<br>66<br>66<br>67  |              | TYPE 2 D   |  | LLLNSLA<br>  | IYLTNRY<br>       <br>IYLTNRY                                    | GIOEGG   |
| US-09-979-603-22<br>US-09-745-842-15<br>US-09-745-842-16<br>US-09-077-173D-2<br>US-09-364-428-60<br>US-09-364-428-60<br>US-09-364-428-60<br>US-09-170-496D-18<br>US-09-170-496D-18<br>US-09-170-496D-18<br>US-09-170-496D-18<br>US-09-170-496D-18<br>US-09-170-496D-18<br>US-08-442-134A-2<br>US-08-442-134A-2<br>US-08-442-134A-2<br>US-08-442-134A-2<br>US-08-442-134A-2<br>US-08-442-134A-2<br>US-08-442-134A-2<br>US-08-443-181B-2<br>US-08-443-181B-2<br>US-08-443-181B-2<br>US-08-443-181B-2<br>US-08-443-181B-2<br>US-08-443-181B-2  | SINTS        |  | 09; DB 2;<br>. 8.1e-132;<br>tches 1;             | VLLVLG<br>   | 00120G   | VARWLL   |
| US-09-979-603:<br>US-09-745-842-<br>US-09-745-842-<br>US-09-077-173D<br>US-09-170-173D<br>US-09-170-496D<br>US-09-170-496D<br>US-09-170-496D<br>US-09-170-496D<br>US-09-170-496D<br>US-09-170-496D<br>US-09-170-496D<br>US-09-170-496D<br>US-09-170-496D<br>US-09-170-496D<br>US-08-442-134A<br>US-08-445-508-<br>US-08-646-618   | AL I GNMENTS | 2869<br>TREATMENT OF<br>09/422,869<br>134,175  | Score 1609; I<br>Pred. No. 8.16<br>); Mismatches | FYAYLG<br>      <br>FYAYLG                                       | rsprpr<br>      <br>rsprpr                                       | LVIGSL   |
| 80-SN<br>60-SN<br>60-SN<br>60-SN<br>60-SN<br>60-SN<br>60-SN<br>60-SN<br>60-SN<br>60-SN<br>60-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN<br>80-SN | ~            | 0942286<br>H S.<br>H S.<br>OF TRE<br>09/09/<br>5-13  | Sc.<br>Pr  | AIKLG  | HSLRD'<br>     <br>HSLRD'  | SAVLWV   |
| 33333333333333333333333333333333333333  |              | 69-20 N. 6235481 NPORMATION: T: POLLONSKY, KENNETH S. T: POLLONSKY, VUKIO T: ODA, NACHISA T: CORN, NANCY J. T: SREENAN, YUKIO T: SREENAN, SEARUS T: ZHOU, YUN-PING T: ZHOU, YUN-PING T: SHEIL, GRAEME I. T: BELL, GRAEME I. T: | 99.6%;<br>ilarity 99.7%;<br>Conservative         | LTWPE  | LPFVI<br>  | AAAVC  |
|   |              | 189-20 18. Application US, 2. 6.25481 INPORMATION: TY: POLONSKY, KENNEY TY: POLONSKY, KENNEY TY: COX, NANCY J. TY: BELL, GRAEME I. TY: GRAEME I. TY: BELL, GRAEME I. TY: GRAEME I. TY: BELL, G | :y<br>ervat                                      | GSSD<br>   |  | RSPRO  |
|   |              | 20 Applicat 235481 RMATION: POLOMSKY, POLOMSKY, ODA, NAOH COX, NANC SRENAN, ZHOE, VUN COX, NANC SRENAN, ZHOE, VUN COX, NANC SRESAN, ZHOE, NANC SRESAN, ZHOEN | Similarity<br>18; Conser                         | TAXT<br>HINT   | VADE<br>VADE   | ARGL:  |
|   |              | 9-20 6.35481 6.255481 FPORMATION FPORMATION FOR CONSTRUCTOR FOR CONSTRUCTOR FREENA FRE | Sim<br>8;  |  |  |  |
| 316.5<br>316.5<br>316.5<br>311.5<br>311.5<br>311.5<br>310.5<br>310.5<br>310.5<br>310.5<br>310.5<br>310.5<br>310.5<br>310.5<br>310.5<br>310.5<br>310.5<br>310.5<br>310.5   |              | BULT 1  -09-422-869-20  Sequence 20, Application US/( SEMERAL INFORMATION: APPLICANT: POLONEXY, KENNETT APPLICANT: POLONEXY, KENNETT APPLICANT: POLONEXY, KENNETT APPLICANT: ODA, NAOHISA APPLICANT: COX, NAOHISA APPLICANT: COX, NANCY J. APPLICANT: COX, NANCY J. APPLICANT: COX, NANCY J. APPLICANT: COX, NANCY J. APPLICANT: HONIS REBRUGE APPLICANT: HANIS, CRAIG I. APPLICANT: APPLICATION NUMBER: CURRENT FILING DATE: 1999-0. NUMBER OF SEQ ID NOS: 30  SEQ ID NO 20 LENGTH: 309 TYPE: PRT CRABALISM: HUMAN ORGANISM: HUMAN -09-422-869-20  | atch<br>cal<br>30                                | <b>н</b> н   | 61   | 121  |
| 0 0 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 0 0 0   |              |  | Query M<br>Best Lo<br>Matches                    |  |  |  |
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APPLICANT: Behar, Dominic F.,
APPLICANT: Chalmers, Derek T.
APPLICANT: Chalmers, Derek T.
APPLICANT: Lerner, Michael
TITLE OF INVENTION: Human G Protein-Coupled Receptors and Modulators Thereof
TITLE OF INVENTION: For the Treatment of Metabolic-Related Disorders
TITLE OF INVENTION: For the Treatment of Metabolic-Related Disorders
TITLE OF INVENTION: 50.02-02-03-03
FILE REFERENCE: 20.02-02-03-04
CURRENT PAPLICATION NUMBER: 10/096,511
PRIOR PELICATION NUMBER: 06/399,917
PRIOR PELING DATE: 2001-11-27
PRIOR PELING DATE: 2001-07-29
PRIOR PELING DATE: 2001-07-29
PRIOR PELING DATE: 2002-08-19
PRIOR PELING DATE: 2002-08-19
PRIOR PELING DATE: 2002-08-19
PRIOR FILING DATE: 2002-08-19
PRIOR FILING DATE: 2002-08-19
PRIOR FILING DATE: 2002-08-13
NUMBER OF SEQ ID NOS: 161
SEQ ID NO 159
TONNEY: 2002-08-16
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                                                                                          281 TNCFLERPAKIMYPITLCLATINCCPDPFIYYFTLESFQKSFYI-----NAHIRMESLF 334
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 159, Application US/10314048A Patent No. 6902902 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Unett, David J.
APPLICANT: Chen, Ruoping
APPLICANT: Richman, Jeremy
APPLICANT: Connolly, Daniel
APPLICANT: Dang, Huong T.
APPLICANT: Choi, Bryan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lowitz, Kevin P.
Behan, Dominic P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Choi, Bryan
Leonard, James
Hakak, Yaron
Liaw, Chen
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Best Local S
Matches 97
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APPLICANT: Sathe, Ganesh
APPLICANT: Van Horn, Stephanie
APPLICANT: Van Horn, Stephanie
APPLICANT: Was down, Derk
APPLICANT: Bague, Derk
APPLICANT: Baguences: 2
CORRESPONDENCE ADDRESS: 2
CORRESPONDENCE ADDRESS: 3
CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSEE: SmithKline Beecham
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: UGA
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241 LAVGWNACALLETIRRALYITSKLSDANCCLDAICYYYMAKBFQEASALAVAPRAKAHKS 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     141 WVLVIGSLVARWLLGIQE-----GGFCFRSTRHNFNSMR--FPLLGFYLPLAVVVF 189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: PA
COMPUTER: PA
COMPUTER: BASADBLE FORM:
MEDLUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
SOFTWARE: PASSESC for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,250
FILING DATE: 10-10-1997
CLASSIFICATION S14
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 34,344
REPERENCE/AGENT INFORMATION:
NAME: WILLIAM T. Han,
RECESTATION NUMBER: 34,344
REPERENCE/DOCKET NUMBER: 34,344
REPERENCE/DOCKET NUMBER: ATGSO043
TELLEPHONE: 610-270-519
                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/08781250
Patent No. 6010877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 34.1%;
Matches 103; Conservative 66
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LENGTH: 370 amino acids
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STRANDEDNESS: single
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MOLECULE TYPE: protein
                                                                      301 QDSLCVTLA 309
                                                                                                                                                 301 ÓDSĽĆVŤĽÁ 309
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264 QNCEVYRSVDLAFFITLSFTYMNSMLDPVVYYFSSPSF 301

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APPLICANT: Lowitz, Kevin P.
APPLICANT: Lowitz, Kevin P.
APPLICANT: Chalmers, Derek T.
APPLICANT: Chalmers, Derek T.
APPLICANT: Lerner, Michael
APPLICANT: Lerner, Michael
TITLE OF INVENTION: Human G Protein-Coupled Receptors and Modulators Thereof
TITLE OF INVENTION: Low the Treatment of Metabolic-Related Disorders
TITLE OF INVENTION: Low DATE: 2002-12-06
FILE REPERENCE: 22.045.CIP
CURRENT APPLICATION NUMBER: US/10/314,048A
CURRENT APPLICATION NUMBER: 00/995,511
PRIOR FILING DATE: 2002-03-12
PRIOR FILING DATE: 2002-07-29
PRIOR FILING DATE: 2002-07-29
PRIOR FILING DATE: 2002-07-29
PRIOR FILING DATE: 2002-08-19
PRIOR FILING DATE: 2002-09-13
PRIOR FILING DATE: 2002-09-13
NUMBER OF SEQ ID NOS: 161
SEQ ID NO 36
LENGTH: 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           94 KPGDIP-CRLMLFMRAMRQGSIIFLTVVAVDRYFRVVHPHHALNKISNRTAAIISCLLW 152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VTALAQRPPTDVGQAEATRKAKR---MVWANLLVFVVCFLPLHVGLTVRLAVGW----- 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          212 IWSLRQR-----QMDRHAKIKRAITFIMVVAIVFVICFLP---SVVVRIRIFWLLHTSG 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DISDIPLCQLSQGIYLINRYMSISLVIAIAVDRYVAVRHPLRARGLRSPRQAAAVCAVLW 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34 IGLEFIFGLIGNGLALMIFCFHLKSWKSSRIFLFNLAVADFLLIICLPFLADNYVRRWDW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2; Length 363;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23.3%; Score 376.5; DB 2; Length 3
34.8%; Pred. No. 6.3e-25;
ive 45; Mismatches 104; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           246 -NACALLETIRRALYITSKLSDANCCLDAICYYYMAKEF 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | : :: | :| : | : | : | TONCEVYRSVDLAFFITLSFTYMNSMLDPVVYYFSSPSF 301
; Sequence 36, Application US/10314048A; Patent No. 6902902
                                                                                                               Richman, Jeremy
Connolly, Daniel
                                                                                                                                                         Dang, Huong T.
Choi, Bryan
Leonard, James
Hakak, Yaron
Liaw, Chen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97; Conservative
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US-09-170-496D-222
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Best Local (
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Sequence 222, Application US/09170496D Patent No. 6555339

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APPLICANT: Behan, Dominic P.
APPLICANT: Behan, Dominic P.
APPLICANT: Chalmers, Derek T.
APPLICANT: Liaw, Chen W.
TITLE OF INVENTION: No. 6555339-Endogenous, Constitutively Activated Human G Protein-CTITLE OP INVENTION: Receptors
FILE REFERENCE: AREN-0040
CURRENT APPLICATION NUMBER: US/09/170,496D
CURRENT FILING DATE: 1998-10-13
NUMBER OF SEQ ID NOS: 294
SOFTWARE: Patentin version 3.1
SEQ ID NO 222
LENGTH: 387
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APPLICANT: Behan, Dominic P.
APPLICANT: Liaw, Chen W.
APPLICANT: Liaw, Chen W.
TITLE OF INVENTION: Receptors
FILE REFERENCE: AREN-0040
CUBRENT APPLICATION NUMBER: US/09/170,496D
CUBRENT FILING DATE: 1998-10-13
NUMBER OF SEQ ID NOS: 294
SOFTWARE: Patentin Version 3.1
SEQ ID NO 108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         87 PL----COLSQGIYLTNRYMSISLVTAIAVDRYVAVRHPIRARGIRSPROAAAVCAVLWV 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    143 LVIG---SLVARWILGIQEG--GFCFR-STRHNF--NSMRFPLIGFYLPLAVVVFCSLKV 194
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23.2%; Score 374.5; DB 2; Length
Best Local Similarity 34.4%; Pred. No. 1e-24;
Matches 95; Conservative 47; Mismatches 107; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        248 CALLETIRRALYITSKLSDANCCLDAICYYYMAKEF 283
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US-09-170-496D-108
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US-09-170-496D-108
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APPLICANT: Benan, Dominic r.

APPLICANT: Chalmers, Derek T.

APPLICANT: Chalmers, Derek T.

APPLICANT: Lerner, Michael

TITLE OF INVENTION: Human G Protein-Coupled Receptors and Modulators Thereof

TITLE OF INVENTION: for the Treatment of Metabolic-Related Disorders

FILE REPERENCE: 22.056.CIP

CURRENT APPLICATION NUMBER: 10506,511

FRICH FILING DATE: 2001-10-27

FRICH REPLING DATE: 2001-11-27

FRICH RILING DATE: 2001-11-27

FRICH RILING DATE: 2001-11-27

FRICH RILING DATE: 2001-07-29

FRICH RILING DATE: 2002-09-13

FRICH RILING DATE: 2002-09-13

FRICH FILING DATE: PAREAULING SATE PAREAULING SA
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APPLICANT: CAO, LIANG
APPLICANT: GENTZ: REINER
APPLICANT: GENTZ: REINER
APPLICANT: GENTZ: REINER
APPLICANT: SULTY CAROL J.
APPLICANT: FOSEN, CRAIG A.
TITLE OF INVENTION: Polymucleotides Encoding Human G-Protein
TITLE OF INVENTION: Coupled Receptor GFRZ
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: STEPNY
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REPAIREMENT OF STEPN
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                                                                                                                                              Lowitz, Kevin P.
Behan, Dominic P.
         Leonard, James
                                                      Hakak, Yaron
Liaw, Chen
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ORGANISM: Homo sapiens
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APPLICANT:
APPLICANT:
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Best Local S:
Matches 98,
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                                                                                                                                                                                      153 GITVGLTVHLLKKKKLL-IQNGPANVCISFSICHTFRWHEAMF-LLEFLLPLGIILFCSAR 210
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94 NFGDIP-CRLVLFMFAMNRQGSIIFLTVVAVDRYFRVVHPHHALNKISNWTAAIISCLLM 152
                                                                                             142 VLVIG---SLVARWLLGIQEG--GFCFR-STRHNF--NSMRFPLLGFYLPLAVVVFCSLK 193
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GENERAL INFORMATION:
APPLICANT: Boehringer Ingelheim Pharma KG
TITLE OF INVERTION: Method for identifying substances which positively
TITLE OF INVENTION: Method for identifying substances which positively
TITLE OF INVENTION: Mifluence inflammatory conditions of chronic
TITLE OF INVENTION: inflammatory airway diseases
TITLE OF INVENTION: inflammatory airway diseases
CURRENT APPLICATION NUMBER: US/09/944,807
CURRENT FILING DATE: 2001-08-31
PRIOR PAPLICATION NUMBER: UK 0021464.1
PRIOR PILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn Ver. 2.1
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;; Pred. No. 2.7e-24;
45; Mismatches 102; Indels 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    262 GTQNCEVYRSVDLAFFITLSFTYMNSMLDPVVYYFSSPSF 301
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Patent No. 6902902
GENERAL INFORMATION:
APPLICANT: Unett, David J.
APPLICANT: Chen, Ruoping
APPLICANT: Connolly, Daniel
APPLICANT: Connolly, Daniel
APPLICANT: Connolly, Daniel
APPLICANT: Conic Sryan
APPLICANT: Choi, Bryan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 21, Application US/09944807
Patent No. 6773895
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Best Local Similarity 35.0%
Matches 98; Conservative
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ORGANISM: Homo sapiens
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US-10-314-048A-135
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US-09-944-807-21
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LENGTH: 387
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TOPOLOGY:
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                                                                                                             COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          125 RGLRSPROAAAVCAVLWVLVI-GSLVARWLLGIQEGG----FCFRSTRHNFNSMRFP-- 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                176 TWKTYLSRIVIFIEIVGFFIPLILAVICSSMVLKTLTK--PVTLSRSKINKTKVLKMIFV 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            222 NLLVPVVCFLPLHVGLTVRLAVGWNA---CALLETIRRALYITSKLSDANCCLDAICYYY 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---LLGFYLPLAVVVPCSLKVVTALAQRPPTDVGQAEATR-KAKRMVWA 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10 SSDLTWPPAIXLGFYAYL-GVLLVLGLLLNSLALWVFCCRMQQWTETRIYMTNLAVADLC 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6 SSHCFYNDSFKYTLYGCMFSMVFVLGLISNCVALYIFICVLKVRNETTTYMINLAMSDLL 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        43;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 344;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22.3%; Score 360.5; DB 1; Length 3
29.2%; Pred. No. 1.4e-23;
tive 68; Mismatches 107; Indels
                                                                                                                           CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/467,948A

FILING DATE: 06-JUN-1995

CLASSIFICATION: 435

PRIOR APPLICATION WHERE: US/08/5/04079

FILING DATE: 06-JUN-1995

APPLICATION WHERE: PCT/US95/04079

FILING DATE: 30-MAR-1995

ATTORNEY/AGENT INFORMATION:
NAME: STEPER, EMIC K.

REGISTRATION NUMBER: 36,688

REGISTRATION NUMBER: 36,688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: LI, YI
APPLICANT: CAO, LIANG
APPLICANT: NI, JIAN
APPLICANT: GENTZ, REINER
APPLICANT: GENTZ, REINER
APPLICANT: SUTTYON III, GRANGER G.
APPLICANT: ROSEN, CRAIG A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 8, Application US/08467947A Patent No. 6090575 GENERAL INFORMATION:
                                                                              MEDIUM TYPE: FLOPPY DISK COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS
                                                                                                                                                                                                                                                                                                                                TELECONMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 344 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                       : 344 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 29.2
Matches 90; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein
                                                              COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  279 MAKEFQEA 286
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WASHINGTON
                                 USA
                                                20005
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 10
US-08-467-947A-8
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69 LLCTLPFVLHSLRDTSDTP----LCQLSQGIYLTNRYMSISLVTAIAVDRYVAVRHPLRA 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 125 RGLRSPRQAAAVCAVLWVLVI-GSLVARWLLGIQEGG-----FCFRSTRHNFNSMRFP-- 176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -LIGFYLPLAVVVFCSLKVVTALAQRPPTDVGQABATR-KAKRMVWA 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 SSHCFYNDSFKYTLYGCMFSMVFVLGLISNCVAIYIFICVLKVRNETTTYMINLAMSDLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10 SSDLTWPPAIKLGFYAYL-GVLLVLGLLLNSLALWVFCCRMQOWTETRIYMTNLAVADLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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TITLE OF INVENTION: Coupled Receptor GPR1
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSE: STENE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVE., NW, SUITE 600
CITY: WASHINGTON
STATE: DC
                                                                                                                                                                                                                                                                      MEDION TIESE FLOCKY

COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/467,947A

FILING DATE: 06-JUN-1995

CLASSIFICATION NUMBER: PCT/US95/04079

FILING DATE: 30-MAR-1995

ATTORNEY/AGENT INFORMATION:

NAME: STEFFE, REIC K.

REGISTRATION NUMBER: 36,688

REFERENCE/DOCKET NUMBER: 1488.1140002/EKS/KLM

TELECOMMUNICATION INFORMATION:

TELEPRAK: 202-371-2540

TELEPRAK: 202-371-2540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22.3%; Score 360.5; DB 2;
29.2%; Pred. No. 1.4e-23;
tive 68; Mismatches 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 4, Application US/09875076; Patent No. 6869776; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : 344 amino acids amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 29.24
Matches 90; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Chen, Ruoping
APPLICANT: Dang, Huong T.
APPLICANT: Liaw, Chen W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS
LENGTH: 344 amino aci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
                                                                                                                                                                                                     ZIP: 20005
COMPUTER READABLE FORM:
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179 FSDBLWKGRLLPLVLLAEALGFLLPLAAVVYSSGRVFWTLA-RP--DATQSQRRRKTVRL 235
                                                                      219 VWANILVFVVCFLPIHVGLTV----RLAVGWNACALLETIRRALYITSKLSDANCCLDAI 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         69 LLCTLPFVLHSLRDTSDTP----LCQLSQGIYLTNRYMSISLVTAIAVDRYVAVRHPLRA 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: CAO, LIANG
APPLICANT: NI, JIAN
APPLICANT: GENTZ, REINER
APPLICANT: GENTZ, REINER
APPLICANT: SUTTON III, GRANGER G.
APPLICANT: ROSEN, CRAIG A.
ITTLE OF INVENTION: Coupled Receptor GPRZ
TITLE OF INVENTION: Coupled Receptor GPRZ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22.3%; Score 359.5; DB 1; Length 302; 30.0%; Pred. No. 1.5e-23; tive 64; Mismatches 103; Indels 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & POX P.L.L.C. STREET: 1100 NEW YORK AVE., NW, SUITE 600 CITY: WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATEMIN RELEASE #1.0, VERSION #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,948A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04079
FILING DATE: 30-MAA-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1488.1140003/EKS/KLM
                                                                                                                                                                                                                296 VYYFSAEGFRNTLRGLGTPHRAR 318
                                                                                                                                                                              275 CYYYMAKEFQEA-SALAVAPRAK 296
                                                                                                                                                                                                                                                                                                                                                                     Sequence 30, Application US/08467948A Patent No. 5998164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: STEFFE, ERIC K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 14(
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 302 amino acids
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not relevant
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CAO, LIANG
NI, JIAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: not releva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      65 AASDLLFTLSLPVRLSYYALH-----HWPPPDLLCQTTGAIFOMNMYGSCIFLMLINVD 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 114 RYVAVRHPLRARGLRSPRQAAAVCAVLWVLVIGSLV-----ARWLLGIQEGGFCFRS 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       119 RYAAIVHPLRLRHLRRPRVARLLCLGVWALILVFAVPAARVHRPSRCRYRDLEVRLCFES 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STNSSVLPCPDYRPTHRLHLVVY-SLVLAAGLPLNALALMVFLRALRVHSVVSVYMCNL 64
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APPLICANT: Lin, I-Lin
ITILE REFERENCE: ARENGOGO
CURRENT APPLICATION NUMBER: US/09/675,076
CURRENT APPLICATION NUMBER: US/09/675,076
CURRENT PLILIG DATE: 1999-10-12
PRIOR PILLING DATE: 1999-10-12
PRIOR APPLICATION NUMBER: 60/120,416
PRIOR APPLICATION NUMBER: 60/120,416
PRIOR APPLICATION NUMBER: 60/120,416
PRIOR APPLICATION NUMBER: 60/120,416
PRIOR PLILING DATE: 1999-03-12
PRIOR PLILING DATE: 1999-05-28
PRIOR PLILING DATE: 1999-05-28
PRIOR PLILING DATE: 1999-05-28
PRIOR PLILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 60/136,439
PRIOR APPLICATION NUMBER: 60/136,439
PRIOR APPLICATION NUMBER: 60/136,439
PRIOR APPLICATION NUMBER: 60/136,439
PRIOR APPLICATION NUMBER: 60/137,131
PRIOR APPLICATION NUMBER: 60/137,131
PRIOR PLILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 60/136,633
PRIOR APPLICATION NUMBER: 60/156,633
PRIOR APPLICATION NUMBER: 60/156,633
PRIOR PLILING DATE: 1999-06-29
PRIOR APPLICATION NUMBER: 60/156,535
PRIOR APPLICATION NUMBER: 60/157,291
PRIOR PLILING DATE: 1999-00-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 372;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22.3%; Score 360; DB 2; 33.7%; Pred. No. 1.7e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 33.7
Matches 109; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
CRGANISM: Homo sapiens
US-09-875-076-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 4
LENGTH: 372
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APPLICANT: Chalmers, Derek T.
APPLICANT: Lerner, Michael
TITLE OF INVENTION: Human G Protein-Coupled Receptors and Modulators Thereof
TITLE OF INVENTION: Human G Protein-Coupled Receptors and Modulators Thereof
TITLE OF INVENTION: For the Treatment of Metabolic-Related Disorders
FILER REPERSENCE: 22 US6.CIP
CURRENT APPLICATION NUMBER: US/10/314,048A
CURRENT FILING DATE: 2002-03-12
PRIOR APPLICATION NUMBER: 09/995,543
PRIOR APPLICATION NUMBER: 60/499,917
PRIOR PILING DATE: 2002-07-29
PRIOR PILING DATE: 2002-07-29
PRIOR PILING DATE: 2002-09-19
PRIOR FILING DATE: 2002-09-19
PRIOR FILING DATE: 2002-09-19
PRIOR FILING DATE: 2002-09-13
NUMBER OF SEQ ID NOS: 161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     143 LVIG----SLVARWILGIQEGGFCFR-STRHNP--NSWRFPLLGFYLPLAVVVFCSLKVV 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     196 TALAQRPPTDVGQAEATRKAKR---MVWANLLVFVVCFLPLHVGLTVRLAVGW----- 245
                                                                                                                                               110 STWKTYLSRIVIPIEIVGFFIPLILMVTCSTMVLRTL-NKPLTLSRNKLSKKKVLKMIFV 228
                                                                                                                                                                                                                            61 FVFTLPFRIYYF-VVRNWPFGDVLCKISVTLFYTNMYGSILFLTCISVDRFLAIVHPFRS 119
                                                                       177 ------LIGFYLPLAVVVFCSLKVVTALAQRPPTDVGQAEATRKAKRMVWA 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31 IGLEFVEGLIGNGLALMIFCFHIKSWKSSRIFLENLAVADFLLICLPFLTDNYVHNWDW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27 IGVLLVLGLLINSLALWVFCCRMQQWTETRIYMTNLAVADLCLLCTLPFVLHSLRDTSDT
                                                                                                                                                                                                     222 NILVEVVCFLPLHVGL---TVRLAVGWNACALLETIRRALYITSKLSDANCCLDAICYYY
                                            125 RGLRSPRQAAAVCAVLWVLVI-GSLVARWLLGIQEGGFCFRST-RHNFNSMR----FP-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Score 348.5; DB 2;
; Pred. No. 1.7e-22;
43; Mismatches 112;
                                                                                                                                                                                                                                                                                                                                            Sequence 137, Application US/10314048A Patent No. 6902902 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 21.6%
Best Local Similarity 33.1%
Matches 92; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lowitz, Kevin P.
Behan, Dominic P
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Connolly, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Unett, David J. APPLICANT: Chen, Ruoping
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Hakak, Yaron
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Chen
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                                                                                                                                                                                                                                                                                                                               10-314-048A-137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10 SSDLTWPPAIKLGFY-AYLGVLLVIGLLLNSLALWVFCCRMQQWTETRIYMTNLAVADLC 68
                                                                                                             170 STWKTYLSRIVIFIEIVGFFIPLILNVTCSTMYLRTL-NKPLTLSRNKLSKKKVLKMIFV 228
                                                                                                                                                                    NLLVEVVCFLPLHVGL----TVRLAVGWNACALLETIRRALYITSKLSDANCCLDAICYYY 278
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                                   RGLRSPROAAAVCAVLWVLVI-GSLVARWLLGIQEGGFCFRST-RHNFNSMR-----FP- 176
                                                                                          ----LLGFYLPLAVVVFCSLKVVTALAQRPPTDVGQAEATRKAKRMVWA 221
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                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: NI, JIAN
APPLICANT: GENTZ, REINER
APPLICANT: GENTZ, REINER
APPLICANT: BULT, CAROL J.
APPLICANT: SUTTON III, GRANGER G.
APPLICANT: ROSEN, CRAIG A.
TITLE OF INVENTION: Polynuclectides Encoding Human G-Protein
TITLE OF INVENTION: Coupled Receptor GPR1
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 302;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C. 1100 NEW YORK AVE., NW, SUITE 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: TEMPEY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,947A
FILING DATE: 06-UN-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: PCT/US95/04079
FILING DATE: 30-MAR-1995
ATCHNEY AGENT INFORMATION:
NAME: STEFFE, ERIC K.
REGISTRATION NUMBER: 36,68
REFERENCE/DOCKET NUMBER: 1488.1140002/EKS/KLM
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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US-08-467-947A-30
i Sequence 30, Application US/08467947A
j Eatent NO. 6090575
j GENERAL INPORMATION:
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INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 302 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 30.0°
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
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CAO, LIANG
NI, JIAN
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COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY
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APPLICANT:
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                125
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APPLICANT: Lowitz, Chain P.
APPLICANT: Lowitz, Kevin P.
APPLICANT: Behan, Dominic P.
APPLICANT: Chalmers, Derek T.
APPLICANT: Chalmers, Derek T.
APPLICANT: Lerner, Michael
TITLE OF INVENTION: Human G Protein-Coupled Receptors and Modulators Thereof
TITLE OF INVENTION: For the Treatment of Metabolic-Related Disorders
TITLE OF INVENTION: 22.056.CIP
TITLE OF INVENTION: 22.056.CIP
TITLE OF INVENTION: 22.056.CIP
CURRENT APPLICATION NUMBER: 10/096,511
PRIOR FILING DATE: 2002-012-06
PRIOR PELLOR NUMBER: 09/995,543
PRIOR FILING DATE: 2002-011-27
PRIOR FILING DATE: 2002-01-1-27
PRIOR FILING DATE: 2002-01-1-27
PRIOR FILING DATE: 2002-01-1-27
PRIOR FILING DATE: 2002-09-13
PRIOR FILING DATE: 2002-09-13
PRIOR SEQ ID NOS: 161
210 WSLRQR------QMDRHAKIKRAINFINVAIVFIICFLP---SVAVRIRIFWLLYKYNV 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          76 -VLHSLRD----TSDTPLCQLSQGIYLTNRYMSISLVTAIAVDRYVAVRHPLRARGLRSP 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    131 ROAAAVCAVLWVLVIGSLVARWLLGIQEGGFCFR-----STRHNFNSMRFPLLG 179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        248 RLYFLWTVPSSACD--PSVHIALHVTLSLTYLNSMLDPLVYYPSSPSFPKFYAKLKIRSL 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16 PPAINLGFYAYLGVLLVIGLLLNSLALMVFCCRMQQMTETRIYMTNLAVADLCLLCTLPF 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21.1%; Score 340.5; DB 2; Length 351;
33.2%; Pred. No. 8e-22;
tive 48; Mismatches 114; Indels 53; Gaps
                                                                                              261 RNCDIYSSVDLAFFTTLSFTYMNSMLDPVVYYFSSPSF 298
                                                                 246 NACALLETIRRALYITSKLSDANCCLDAICYYYMAKEF 283
                                                                                                                                                                                                            Sequence 157, Application US/10314048A
Patent No. 6902902
GENERAL INFORMATION:
APPLICANT: Unett, David J.
APPLICANT: Chen, Ruoping
APPLICANT: Richman, Jeremy
APPLICANT: Connolly, Daniel
APPLICANT: Dang, Huong T.
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Best Local Similarity 33.24
Matches 107; Conservative
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Leonard, James
Hakak, Yaron
Liaw, Chen
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US-10-314-048A-157
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Search completed: February 9, 2006, 01:02:28 Job time : 34.5 secs

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351, Appl
351, Appl
351, Appl
44, Appl
225, App
176, App
111, Appl
111, Appl
1176, Appl
1176, Appl
1176, Appl
110, Appl
10, Appl
10, Appl
1174, Appl
1174,
                                                                                                         9, 2006, 01:16:44; Search time 118.5 Seconds (without alignments) 1089.530 Million cell updates/sec
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(cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
(cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
(cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
(cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
(cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
(cgn2_6/ptodata/1/pubpaa/US111_PUBCOMB.pep:*)
GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd
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US-10-225-567A-492
US-10-255-567A-492
US-10-505-486-84
US-10-157-031-351
US-10-09-964-821B-11
US-10-024-298A-176
US-10-268-332-11
US-10-268-332-11
US-10-268-332-11
US-10-268-332-11
US-10-268-332-11
US-10-268-332-11
US-10-024-298A-176
US-10-024-298A-176
US-10-024-298A-174
US-10-024-298A-174
US-10-024-298A-174
US-10-268-332-10
US-10-024-298A-174
US-10-024-298A-174
US-10-031-048-159
US-10-314-048A-159
US-10-313-16
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                                                                                                                                                                                                                                                                                                                      1867569 seqs, 417829326 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                             model
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Gapop 10.0 , Gapext 0.5
                                                                             using sw
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length: 200000000
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1615
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                                                                                                                 February
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Match 1
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Maximum DB seq
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                                                                                                                                                                                                              score:
                                                                               protein
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                                                                                                                                                                 Score 1609; DB 5; Length 309;
Pred. No. 6.9e-147;
0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 84, Application US/10505486
| Publication No. US20050118639A1
| GENERAL INFORMATION:
| APPLICANT: Takeda Chemical Industries, Ltd.
| TITLE OF INVENTION:
| FILE REFERENCE: PO3-0006PCT
| CURRENT PILLING DATE: 2004-08-20
| PRIOR APPLICATION NUMBER: US/10/505,486
| CURRENT FILING DATE: 2002-02-22
| PRIOR FILING DATE: 2002-02-23
| PRIOR FILING DATE: 2002-07-3
| PRIOR FILING DATE: 2002-07-3
| PRIOR PILING DATE: 2002-10-11
| NUMBER OF SEQ ID NOS: 233
| SEQ ID NO 84
                                                                                                                                                                        99.64;
                         PatentIn version 3.1
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Matches 308; Conservative
    NUMBER OF SEQ ID NOS: 3114
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                                                                                                       ; ORGANISM: homo sapiens
US-10-696-639-44
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ORGANISM: Human
                     SOFTWARE: Pate
SEQ ID NO 44
LENGTH: 309
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                                                                                      TYPE: PRT
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Best Local S
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                                                                                                                                                           Sequence 44, Application US/10696639
Publication No. US20050037439A1
GENERAL INFORMATION:
APPLICANT: Bourner, Maureen J.
TITLE OF INVENTION:
PLICANT: BOURNER, MAURENTIALLY EXPRESSED GENES INVOLVED IN CANCER, THE
TITLE OF INVENTION: POLYPEPTIDES ENCODED THEREBY, AND METHODS OF USING THE SAME
FILE REFERENCE: 01040/1
CURRENT APPLICATION NUMBER: US/10/696,639
CURRENT PLING DATE: 2003-10-29
PRIOR APPLICATION NUMBER: 60/422,176
PRIOR FILING DATE: 2002-10-29
241 LAVGWNACALLETIRRALYITSKLSDANCCLDAICYYYMAKBFQBASALAVAPRAKAHKS 300
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Pred. No. 6.9e-147;
0; Mismatches 1; Indels
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Best Local Similarity 99.7%;
Matches 308; Conservative (
                                                                                  301 ODSLCVTLA 309
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                                      301 ODSLCVTLA 309
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ORGANISM: Homo sapiens
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LENGTH: 309
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APPLICANT: BARBER, I.
APPLICANT: BARBER, M. G.
TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPRBMY3,
TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RELATED TISSUES
TITLE OF INVENTION: EXPRESSED HIGHLY IN IMMUNE- AND COLON- RELATED TISSUES
FILE REFERENCE: D0042NP
CURRENT APPLICATION NUMBER: 06/0235, 713
PRIOR FILING DATE: 2000-09-27
PRIOR FILING DATE: 2001-01-17
PRIOR PLICATION NUMBER: 60/235, 73
PRIOR FILING DATE: 2001-01-17
PRIOR FILING DATE: 2001-01-17
PRIOR FILING DATE: 2001-00-17
PRIOR FILING DATE: 2001-00-17
PRIOR FILING DATE: 2001-00-17
SOFTWARE: PLANCE DATE: 2001-08-17
NUMBER OF SEQ ID NOS: 63
SOFTWARE: PATENTIN VET: 2.1
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Best Local Similarity 34.1%
Matches 103; Conservative
MINTIER, G.
RAMANATHAN, C.
HAWKEN, D.R.
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| Sequence 351, Application US/10157031
| Publication No. US20030108890A1
| GENERAL INFORMATION:
| APPLICANT: Baranova, A. V. | APPLICANT: Yankovsky, N. K. |
| APPLICANT: Lobashev, A. P. | APPLICANT: Lobashev, A. P. | APPLICANT: Kralov, A. P. | APPLICANT: Tubashev, A. V. | APPLICANT: APPLICANT: Consensual Consens
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YLPLAVVVPCSLKVVTALAQRPPTDVGQAEATRKAKRMVWANLLVFVVCFLPLHVGLTVR 240
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ORGANISM: Homo sapiens
US-10-157-031-351
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Best Local Similarity
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163 WILVLSGGISASLESTINVNNATTTCPEGFSKRVWKTYLSKITIFIEVVGFIIPLILNVS 222
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24.8*; Score 401; DB 4; Length 37
Best Local Similarity 34.1*; Pred. No. 4.1e-30;
Matches 103; Conservative 60; Mismatches 111; Indels
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APPLICANT: Shuji MURANATSU
APPLICANT: Shuji MURANATSU
APPLICANT: Yukiko NaGANO
TITLE REPERENCE: 1254-0191P
CURRENT APPLICATION NUMBER: US/10/024,298A
CURRENT FILING DATE: 2003-04-08
PRIOR PILING DATE: 2001-08-24
PRIOR PILING DATE: 2001-08-24
PRIOR PILING DATE: 2000-12-26
PRIOR APPLICATION NUMBER: 60/258,315
PRIOR APPLICATION NUMBER: 60/258,315
PRIOR APPLICATION NUMBER: 10254018/2001
PRIOR PILING DATE: 2000-12-28
PRIOR PILING DATE: 2000-12-28
PRIOR PILING DATE: 2001-08-24
PRIOR PRILING DATE: 2001-08-24
PRIOR PILING DATE: 2001-03-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Publication No. US20030143540A1
GENERAL INPORMATION:
APPLICANT: ASAHI KASER KABUSHIKI KAISHA
APPLICANT: Goichi HONDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 176, Application US/10024298A Publication No. US20030143540A1
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CRGANISM: Homo sapiens
US-10-024-298A-176
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APPLICANT: Burmer, Glenna C.
APPLICANT: Burmer, Glenna C.
APPLICANT: Roush, Christine L.
TITLE OF INVENTION: ANTIGENE PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS FILE REFRENCE: 1920-4-4
GURRENT APPLICATION NUMBER: US/10/225,567A
CURRENT FILING DATE: 2001-12-19
PRIOR PILING DATE: 2000-12-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               223 CSSVVLRTL--RKPATLSQIGTNKKKVLKMITVHMAVFVVCFVPYNSVLFLYALVRSQAI 280
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24.8%; Score 401; DB 4; Length 370;
Best Local Similarity 34.1%; Pred. No. 4.1e-30;
Matches 103; Conservative 60; Mismatches 111; Indels
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APPLICANT: LifeSpan Biosciences
NUMBER OF SEQ ID NOS: 58
SOFTWARE: Patentin version 3.0
SEQ ID NO 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 2292
SOFTWARE: Patentin version 3.1
SEQ ID NO 225
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Matches 103; Conservative
                                                                                                                       ORGANISM: Homo sapiens
US-10-081-810-44
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US-10-225-567A-225
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US-10-225-567A-225
                                                                            LENGTH: 370
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44 AVYSVVPILGLITNSVSLEVPCFRRKÆRSETAIFITNLAVSDLLFVCTLPFKIFYNFNRH 103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           281 TNCFLERFAKIMYPITLCLATLNCCFDPFIXYFTLESFQKSFYI-----NAHIRMESLF 334
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 370;
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24.8%; Score 401; DB 4; Length 37

Best Local Similarity 34.1%; Pred. No. 4.1e-30;

Matches 103; Conservative 60; Mismatches 111; Indels
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PUBLICATION NO. US20040081986A1
GENERAL INFORMATION: Akio et al.
TITLE OF INVENTION: NF-kB ACTIVATING GENE
FILE REFERENCE: 1234-0229P
CURRENT PELING DATE: 2003-07-11
PRIOR REPLICATION NUMBER: US 2000-40228B
PRIOR PELING DATE: 2000-12-28
PRIOR PELING DATE: 2001-03-26
FILE KEFERGER DATE: 100728 1312
CURRENT FILING DATE: 2002-10-10
PRIOR APPLICATION NUMBER: U.S. 60/235,713
PRIOR FILING DATE: 2000-09-27
PRIOR FILING DATE: 2000-09-27
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-07-13
PRIOR FILING DATE: 2001-07-13
PRIOR FILING DATE: 2001-08-17
PRIOR PLING DATE: 2001-08-17
PRIOR PLING DATE: 2001-08-17
PRIOR PLING DATE: 2001-09-26
NUMBER OF SEQ ID NOS: 66
SOFTWARE: PARCHIN VERSION 3: 1
SERVENDER 1: 370
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Sequence 11, Application US/10268332

Sequence 11, Application World 19841

GENERAL INFORMATION:

APPLICANT: Bilstol-Myers Squibb Company

APPLICANT: Bilstol-Myers Squibb Company

TITLE OF INVENTION: IMMUNE- HUMAN G-PROTEIN COUPLED RECEPTOR, HGPRBMY3, EXPRESSED HIGHT

TITLE OF INVENTION: IMMUNE- AND COLON- RELATED TISSUES
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24.8%; Score 401; DB 4; Length 370

Best Local Similarity 34.1%; Pred. No. 4.1e-30;

Matches 103; Conservative 60; Mismatches 111; Indels
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TITLE OF INVENTION, NFKB ACTIVATING Gene
FILE REFERENCE: 1254-0192P
CURRENT APPLICATION NUMBER: US/10/042,211A
CURRENT PELING DATE: 2002-01-11
PRIOR PILING DATE: 2000-12-28
PRIOR PILING DATE: 2001-03-26
PRIOR PILING DATE: 2001-03-26
PRIOR PILING DATE: 2001-03-26
PRIOR PILING DATE: 2001-08-24
PRIOR PILING DATE: 2001-03-26
PRIOR FILING DATE: 2001-03-26
PRIOR FILING DATE: 2001-03-26
PRIOR FILING DATE: 2001-03-26
PRIOR PILING DATE: 2001-03-26
                                                                                                                                                                                                                                    ; Sequence 176, Application US/10042211A; Publication No. US20030170719A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Homo sapiens
US-10-042-211A-176
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                          VT 307
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223 CSSVVLRTL--RKPATLSQIGTNKKKVLKMITVHMAVFVVCFVPYNSVLFLYALVRGAI 280
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                                                                                                                                                     281 TNCFLERPAKIMYPITLCLATLNCCFDPFIYYPTLESFQKSFYI-----NAHIRMESLF 334
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     190 CSLKVVTALAQRPPTDVGQAEAT-RKAKRMVWANLLVFVVCFLPLHVGLTVRLAVGWNAC 248
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24.8%; Score 401; DB 4; Length 37'
Best Local Similarity 34.1%; Pred. No. 4.1e-30;
Matches 103; Conservative 60; Mismatches 111; Indels
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APPLICANT: Golichi HONDA
APPLICANT: Shuji MURAMATSU
APPLICANT: Yakiko NAGANO
TITLE OF INVENTION: NF-K B ACTIVATING Gene
FILE REFERENCE: 1254-0191P
CURRENT FILING DATE: 2003-04-08
PRIOR APPLICATION NUMBER: 60/314,385
PRIOR APPLICATION NUMBER: 60/314,385
PRIOR APPLICATION NUMBER: 60/278,641
PRIOR PILING DATE: 2001-08-24
PRIOR PILING DATE: 2001-03-26
PRIOR PILING DATE: 2000-12-28
PRIOR PILING DATE: 2001-03-24
PRIOR PILING DATE: 2001-03-24
PRIOR PILING DATE: 2001-03-24
PRIOR PILING DATE: 2001-03-24
PRIOR PILING DATE: 2001-03-26
PRIOR PILING DATE: 2000-12-38
SOFTWARE: PATENTING NUMBER: JP402288/2000
SEQ ID NOS: 182
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APPLICANT: Akio MATSUDA
                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 176, Application US/10024298APublication No. US20040214167A9GENERAL INFORMATION:
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US-10-024-298A-176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 11, Application US/10775965
Publication No. US20040209808A1
GENERAL INFORMATION:
APPLICANT: Bristol-Wers Squibb Company
APPLICANT: Rornacker, Michael
ITILE OF INVENTION: MODULATORS OF HUMAN G-PROTEIN COUPLED RECEPTORS
FILE REPERENCE: DOZSE NP
CURRENT APPLICATION NUMBER: US/10/775,965
CURRENT APPLICATION NUMBER: US. 60/446,655
PRIOR FILING DATE: 2003-02-11
PRIOR FILING DATE: 2003-02-11
NUMBER OF SEQ ID NOS: 112
SOFTWARE: Patentin version 3.2
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24.8%; Score 401; DB 4; Length 370;
Best Local Similarity 34.1%; Pred. No. 4.1e-30;
Matches 103; Conservative 60; Mismatches 111; Indels
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24.8%; Score 401; DB 4; Length 370;
Best Local Similarity 34.1%; Pred. No. 4.1e-30;
Matches 103; Conservative 60; Mismatches 111; Indels
SOPTWARE: Patentin Ver. 2.0
SEQ ID NO 176
LENGTH: 370
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ORGANISM: Homo sapiens
US-10-775-965-11
                                                                                                         ORGANISM: Homo sapiens
US-10-617-217A-176
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US-10-775-965-11
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Search completed: February
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24.8%; Score 401; DB 5; Length 370;
Best Local Similarity 34.1%; Pred. No. 4.1e-30;
Matches 103; Conservative 60; Mismatches 111; Indels 28; Gaps
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                                                                                                                                                       Sequence 86, Application US/10753267
Publication No. US20050037946A1
APPLICANT: Millennium Pharmaceuticals, Inc.
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KT 336
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        Qy
        190 CSLKVVTALAQRPPTDVGQAEAT-RKAKRWWANLLVFVVCFLPLHVGLTVRLAVGWNAC 248

        Db
        223 CSSVVLTTL--RKPATLSQIGTNKKKVLKMITVHMAVFVSCVFVNSVLFLYALVRSQAI 280

        Qy
        249 --ALLETIRRALY-ITSCADANCCCADAICYVRAKEQEGASALAVAPRAKKGDSLC 305

        Db
        281 TNCFLERFAKIMYPITLCLATLNCCFDPFIYYFTLESFQKSFYI-----NAHIRMESLF 334

        Qy
        306 VT 307

        Db
        335 KT 336
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9, 2006, 01:21:15

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February 9, 2006, 01:17:29; Search time 10.5 Seconds (without alignments) 386.178 Million cell updates/sec
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1615
1 MNGTYNTCGSSDLTWPPAIK......AVAPRAKAHKSQDSLCVTLA 309
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1: /cgn2_6/ptodata/1/pubpaa/US08 NEW PUB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/US06 NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US07 NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US10 NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US10 NEW_PUB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/US10 NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/US10 NEW_PUB.pep:*
GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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Maximum Match 100%
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Gapop 10.0 , Gapext 0.5
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SIMMARIE

|           |        | Description     | 248,              | 327,              | 340               | 83               | Seguence 2, Appli | 545               |                  | 225,              |                   | Sequence 4, Appli | Ġ               | Sequence 66, Appl | Sequence 46, Appl | Sequence 523, App | Sequence 2, Appli | Sequence 61, Appl | 20    | Sequence 5, Appli | Sequence 67, Appl | 62, A            | 712,              | Sequence 716, App | Ā               | ⋖,               | Sequence 713, App |
|-----------|--------|-----------------|-------------------|-------------------|-------------------|------------------|-------------------|-------------------|------------------|-------------------|-------------------|-------------------|-----------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------|-------------------|-------------------|------------------|-------------------|-------------------|-----------------|------------------|-------------------|
| SUMMARIES |        | ai<br>T         | US-10-055-877-248 | US-10-055-877-327 | US-10-055-877-340 | US-10-877-346-83 | US-11-157-930-2   | US-10-995-561-545 | US-11-127-877-52 | US-10-055-877-225 | US-10-055-877-237 | US-11-157-930-4   | US-11-157-930-6 | US-11-127-877-66  | US-11-127-877-46  | US-10-995-561-523 | ᅼ                 | US-11-127-877-61  | н     | US-11-157-930-5   | US-11-127-877-67  | US-11-127-877-62 | US-10-995-561-712 | US-10-995-561-716 | US-10-876-787-2 | US-11-127-877-65 | US-10-995-561-713 |
|           |        | e :             | 9                 | ø                 | ø                 | 9                | 7                 | 9                 | 7                | 9                 | 9                 | 7                 | 7               | 7                 | 7                 | 9                 | 7                 | 7                 | 7     | 7                 | 7                 | 7                | 9                 | 9                 | 9               | 7                | 9                 |
|           |        | Match Length DB | 254               | 254               | 254               | 254              | 346               | 365               | 391              | 259               | 259               | 339               | 367             | 358               | 373               | 352               | 352               | 352               | 352   | 337               | 375               | 374              | 359               | 359               | 359             | 359              | 388               |
|           | Query  | Match           | 20.4              | 20.4              | 20.4              | 20.4             | 19.6              | 19.5              | 19.3             | 18.6              | 18.6              | 18.5              | 18.5            | 18.4              | 18.4              | 17.7              | 17.7              | 17.7              | 17.7  | 16.9              | 16.9              | 16.2             | 15.8              | 15.8              | 15.8            | 15.8             | 15.8              |
|           |        | Score           | 329.5             | 329.5             | 329.5             | 329.5            | 316.5             | 315.5             | 311.5            | 300               | 300               | 298               | 298             | 297.5             | 296.5             | 286.5             | 286.5             | 286.5             | 285.5 | 273.5             | 273.5             | 261.5            |                   | 255.5             | 255.5           | 255.5            | 255.5             |
|           | Result | No.             | -                 | 7                 | m                 | 4                | S                 | 9                 | 7                | 60                | σ                 | 10                | 11              | 12                | 13                | 14                | 15                | 16                | 17    | 18                | 19                | 20               | 21                | 22                | 23              | 24               | 25                |

| Sequence 714, App<br>Sequence 715, App<br>Sequence 55, Appl<br>Sequence 934, Appl |  | Sequence 161, App<br>Sequence 4, Appli<br>Sequence 64, Appl<br>Sequence 4, Appli | 36,<br>12,<br>24,<br>636                           | Sequence 637, App<br>Sequence 6, Appli<br>Sequence 59, Appli<br>Sequence 32, Appl |
|---|--|--|--|---|
| US-10-995-561-714<br>US-10-995-561-715<br>US-11-127-877-55<br>US-110-821-234-934  |  | US-10-055-877-161<br>US-11-068-686-4<br>US-11-127-877-64<br>US-11-216-610-4      | :2555  | US-10-995-561-637<br>US-11-216-610-6<br>US-11-127-877-59<br>US-11-218-281-32      |
| 394 6<br>394 6<br>400 7   | 388 6<br>388 6<br>355 7                          | 355 7<br>355 7   | 351 7<br>351 7<br>351 7<br>355 6                   | 362 6<br>355 7<br>352 7<br>352 7  |
| 255.5 15.8<br>255.5 15.8<br>254 15.7  | 249 15.4<br>249 15.4<br>248.5 15.4<br>246.5 15.3 | 243.5 15.1<br>243.5 15.1<br>243.5 15.1   | 242.5 15.0<br>242.1 14.9<br>241 14.9<br>240.5 14.9 | 240.5 14.9<br>237.5 14.7<br>234.5 14.5<br>234.5 14.5                              |
| 26<br>28<br>28  | 3310   | . w w w u  | . w w 4 4  | 4 4 4 4<br>0 W 4 R  |

## ALIGNMENTS

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US-10 OBS-5877-208-248. Application US/10058977

BUDICATION ON USZO050288241A1

GENERAL HYDORATION

APPLICANT: Dedigary, Muralidhara

APPLICANT: Chernev, Velizar

APPLICANT: Chernev, Velizar

APPLICANT: Chernev, Velizar

APPLICANT: Shory, Misory

APPLICANT: Spytek, Kimberly

APPLICANT: School, Valerie

APPLICANT: School, Valerie

APPLICANT: Chernev, David

APPLICANT: Andrew, David

APPLICANT: Andrew, David

APPLICANT: Andrew, David

APPLICANT: Andrew, David

APPLICANT: Paturial Andrew

APPLICANT: Shimkers, Richard

APPLICANT: Conine

APPLICANT: Shimkers, Richard

APPLICANTS Stoll-0-1-3

FRIOR FILING DATE: 2001-01-25

FRIOR PILING DATE: 2001-01-25

FRIOR PILING DATE: 2001-01-25

FRIOR APPLICATION NUMBER: 60/264,117

FRIOR PILING DATE: 2001-01-25
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RESULT 3
US-10-055-877-340
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   193 KVVTALAQRPPTDVG---QAEATRKAKRMVWANLLVFVVCFLPLHVGLTVRLAVGWNACA 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         144 V----IGSLVARWLLGIQEGG------FCFRSTRHNFNSMRFPLLGFYLPLAVVVFCSL 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28 GVLLVLGLLLNSLALWVFCCRMQQWTETRIYMTNLAVADLCLLCTL-PFVLHSLRD---T 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 60/264,478
PRIOR PILING DATE: 2001-01-26
PRIOR PLING DATE: 2001-01-26
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: 60/275,990
PRIOR PLING DATE: 2001-03-02
PRIOR PLING DATE: 2001-03-14
PRIOR PLING PRIOR APPLICATION NUMBER: 60/275,927
PRIOR PLING DATE: 2001-03-14
PRIOR PLING DATE: 2001-03-14
PRIOR PLING DATE: 2001-03-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 20.4*; Score 329.5; DB 6; Length 254; Best Local Similarity 33.7*; Pred. No. 9.5e-25; Matches 91; Conservative 54; Mismatches 88; Indels 37;
                                                                                                                                                                                                                                                                                                                                                                          PEATURE:
1 OTHER INFORMATION: Description of Artificial Sequence: 7tm_1, 7
1 OTHER INFORMATION: transmembrane receptor domain
18-10-055-877-248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     250 LLETIR---RALYITSKLSDANCCLDAICY 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  225 LLSIWRVLPTALLITLWLAYVNSCLNPIIY 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 327, Application US/10055877 Publication No. US20050288241A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Decristofaro, Marc APPLICANT: Padigaru, Muralidhara APPLICANT: Miler, Charles APPLICANT: Tchernev, Velizar APPLICANT: Zhong, Mei APPLICANT: Anderson, David APPLICANT: Ballinger, Robert APPLICANT: Syrek, Kimberly APPLICANT: Ratelli, Luca APPLICANT: Actusen, Bryan APPLICANT: Zerhusen, Bryan APPLICANT: Andrew, David APPLICANT: Mezes, Peter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Patturajan, Meera
Burgess, Cahterine
Elsen, Andrew
                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Artificial Sequence
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Shimkets, Richard
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US-10-055-877-327
                                                                                                                                                                                                                                                                                        SEQ ID NO 248
LENGTH: 254
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APPLICANT: Shenoy, Suresh
APPLICANT: Shenoy, Suresh
APPLICANT: Shenoy, Suresh
APPLICANT: Casman, Stacie
APPLICANT: Casman, Stacie
APPLICANT: Casman, Stacie
APPLICANT: Casman, Stacie
APPLICANT: Boldog, Ference
TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoded Thereby
TIES REPERENCE: 21402-251
CURRENT APPLICATION NUMBER: 05/262,892
PRIOR PLING DATE: 2001-01-23
PRIOR PLING DATE: 2001-01-24
PRIOR PLING DATE: 2001-01-24
PRIOR PLING DATE: 2001-01-25
PRIOR PLING DATE: 2001-01-26
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2001-03-02
PRIOR PLING DATE: 2001-03-04
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112 ALLLSLPPLLFSWLRTVEEGNTTVCLIDFPEBSVKRSY-VLLSTLVGFVLPLLVILVCYT 170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | | | | :: | : | - ----RTPINIFILINIAVADLLFLITLPPWALYYLVGGDWV 51
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OTHER INFORMATION: transmembrane receptor domain consensus sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  250 LLETIR---RALYITSKLSDANCCLDAICY 276
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Vernet, Corine
Taupier Jr., Raymond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Artificial Sequence
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193 KVVTALAQRPPTDVG----QAEATRKAKRMVWANLLVFVVCFLPLHVGLTVRLAVGWNACA 249
                                                                                                                                   144 V----IGSLVARWILGIQEGG-----FCFRSTRHNFNSMRFPLLGFYLPLAVVVFCSL 192
                                                                                                                                                                                   : |: || || || |: |
112 ALLLSLPPLLFSWLRIVEEGNTIVCLIDFPEESVKRSY-VLLSTLVGFVLPLLVILVCYT 170
                                                                                                                                                                                                                                                                                                                   171 RILKTURKRARSORSLKRRSSSERKAAKMILVVVVVFVICWLPYHIVLLL-----DSLC 224
                                52 FGDALCKLVGAAFEVVNGYASILLLTAISIDRYLAIVHPLRYRRIRTPRRAKVLILLVWVL 111
84 SDTPLCQLSQGIYLTWRYMSISLVTAIAVDRYVAVRHPLRARGLRSPRQAAAVCAVLWVL 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Burgess, Carnerine E
APPLICANT: Burgess, Carnerine E
APPLICANT: Padigaru, Muralidhara
APPLICANT: Servick, Ramesh
APPLICANT: Spytek, Kimberly A
APPLICANT: Shimkets, Richard A
APPLICANT: Leach, Martin D
APPLICANT: Shimkets, Richard A
ITILE OF INVENTION: NOVel Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-124
CURRENT APPLICATION NUMBER: US/10/9964,956
FRIOR PELING DATE: 2001-09-27
FRIOR APPLICATION NUMBER: 60/235,631
FRIOR APPLICATION NUMBER: 60/235,631
FRIOR APPLICATION NUMBER: 60/235,633
FRIOR FILING DATE: 2000-09-27
FRIOR FILING DATE: 2000-09-28
FRIOR FILING DATE: 2000-00-09-28
FRIOR FILING DATE: 2000-00-09-08
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SOFTWARE: PatentIn Ver. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     225 LLSIWRVLPTALLITLWLAYVNSCLNPIIY 254
                                                                                                                                                                                                                                                                                                                                                                                                                             250 LLETIR---RALYITSKLSDANCCLDAICY 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 83, Application US/10877346 Publication No. US20060014153A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ellerman, Karen
Grosse, William M
Alsobrook II, John P
Lepley, Denise M
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Gerlach, Valerie L
APPLICANT: MacDougall, John R
APPLICANT: Smithson, Glennda
APPLICANT: Millet, Isabelle
APPLICANT: Stone, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gunther, Erik
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 83
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APPLICANT: Boldog, Ference
TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoded Thereby
TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoded Thereby
FILE REFERENCE: 2402-251
CURRENT PILING DATE: 2002-01-22
FRIOR APPLICATION NUMBER: 60/262,892
FRIOR PILING DATE: 2001-01-19
FRIOR PILING DATE: 2001-01-24
FRIOR APPLICATION NUMBER: 60/264,117
FRIOR PILING DATE: 2001-01-24
FRIOR PILING DATE: 2001-01-24
FRIOR PILING DATE: 2001-01-25
FRIOR PILING DATE: 2001-01-25
FRIOR APPLICATION NUMBER: 60/264,139
FRIOR PILING DATE: 2001-01-26
FRIOR APPLICATION NUMBER: 60/264,139
FRIOR FILING DATE: 2001-01-26
FRIOR PILING DATE: 2001-01-26
FRIOR APPLICATION NUMBER: 60/263,351
FRIOR APPLICATION NUMBER: 60/263,351
FRIOR APPLICATION NUMBER: 60/272,870
FRIOR FILING DATE: 2001-03-02
FRIOR PILING DATE: 2001-03-14
FRIOR APPLICATION NUMBER: 60/275,990
FRIOR FILING DATE: 2001-03-14
FRIOR FILING DATE: 201-03-14
FRIOR FILING DATE: 201-03-14
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20.4%; Score 329.5; DB 6; Length 254;
Best Local Similarity 33.7%; Pred. No. 9.5e-25;
Matches 91; Conservative 54; Mismatches 88; Indels 37; Gaps
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       DeCristofaro, Marc
Padigaru, Muralidhara
Miller, Charles
Tohernev, Velizar
Zhong, Mei
Anderson, David
Ballinger, Robert
Gerlach, Valerie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Baumgartner, Jason
Shimkets, Richard
Gusev, Vladimir
Vernet, Corine
Taupier Jr., Raymond
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Burgess, Cahterine
Eisen, Andrew
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Zerhusen, Bryan
Andrew, David
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Kekuda, Ramesh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Casman, Stacie
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Andrew, David
Mezes, Peter
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LENGTH: 254
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APPLICANT:
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APPLICANT:
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US-11-127-877-52

US-11-127-877-52

Sequence 52, Application US/11127877

Sequence 52, Application No. US20050287565A1

Sequence 52, Application No. US20050287565A1

GENERAL INFORMATION:
APPLICANT: Merchiers, Pascal G.
APPLICANT: Spittaels, Koenraad F. F.
APPLICANT: Spittaels, Koenraad F. F.
APPLICANT: Laenen, Wendy
ITILE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
ITILE OF INVENTION: Methods USA
ITILE OF INVENTION: MAYLOId-Beta Protein Production
FILE REFERENCE: P27, 800-8 USA
CURRENT PILING DATE: 2005-05-12

PRIOR FILING DATE: 2004-05-12

PRIOR FILING DATE: 2004-05-12
                                                                                                                                                                                                                                   US-10-995-561-545

Sequence 545, Application US/10995561

Sequence 545, Application US/10995561

Publication No. US20050272054A1

GENERAL INPORNATION:

APPLICANT: CARGILL, Michele et al.

TITLE OF INVENTION: CARDICAR DISORDERS AND DRUG RESPONSE, METHODS OF TITLE OF INVENTION: DETECTION AND USES THEREOF

FILE REPERENCE: CLO01559

CURRENT APPLICATION NUMBER: US/10/995,561

CURRENT FILING DATE: 2004-11-24

NUMBER OF SEQ ID NOS: 85702

SOFTWARE: PRESECT OF Windows Version 4.0
44 VVFVLGLGLNAPTLWLFIPRLRPWDATATYMFHLALSDTLYVLSLPTLIYYYAAHNHWPF 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               88 ---LCQLSQGIYLTNRYMSISLVTAIAVDRYVAVRHPLRARGLRSPRQAAAVCAVLWVLV 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    145 IGSLVAR-WLLGIQEGG---PCPRSTR----H--NFNSMRPPLLGFYLPLAVVVFCSLK 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   164 AGCLVPNLFFYTTSNKGTTVLCHDTTRPEEFDHYVHFSSAVMGLL-FGVPCLVTLVCYGL 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       194 VVTALAQRPPTDVGQAEATRKAK--RMVMANILIVPVVCPLPLHVGLTV----RLAVGWNA 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        248 CALLETIRRALYITSKLSDANCCLDAICYYYMAKEFQE------ASALAV 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                278 CRVINIVNVYKVTRPLASANSCLDPVLYLLTGDKYRROLROLCGGGKPOPRTAASSLAL 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29 VLLVIGILINSLALWVPCCRMQQWTETRIYMTNLAVADLCLLCTLPFVLHSLRDTSDTP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19.5%; Score 315.5; DB 6; Length 3
29.2%; Pred. No. 3.2e-23;
tive 56; Mismatches 123; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       292 APRAK-----AHKSQDSLCVT 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        338 VSLPEDSSCRWAATPODSSCST 359
                                                                                  286 -ASALAVAPRAKA 297
                                                                                                                                   316 LKSALRKGHPQKA 328
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-545
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Best Local Similarity
Matches 94; Conservat
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                                                                                                                                                                                                                                                                 84 SDTPLCQLSQGIYLTNRYMSISLVTAIAVDRYVAVRHPLRARGLRSPRQAAAVCAVLWVL 143
                                                                                                                                                                                                                                                                                            144 V----IGSLVARWLLGIQEGG------PCPRSTRHNFNSMRPPLLGFYLPLAVVVPCSL 192
                                                                                                                                                                                                                                                                                                                                                                                                       : |: || || || |: |
112 ALLLSLPPLLFSWLRTVEEGNTTVCLIDPPEESVKRSY-VLLSTLVGFVLPLLVILVCYT 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              193 KVVTALAQRPPTDVG---QAEATRKAKRMVWANLLVFVVCFLPLHVGLTVRLAVGWNACA 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60 TNLAVADLCLLCTLPF-VLHSLRDTS----DTPLCQLSQGIYLTNRYMSISLVTALAVDR 114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 227 VVCFLPLHVGLTVRLAVGWNACALLETIRRALYITSKLSDANCCLDAICYYYMAKEFQE- 285
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                                                                                                                                                                                          1 GNLLVILVILVILKTKKL-----RTPINIFILINIAVADLLFLLTLPPWALYYLVGGDWV 51
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                                                                                                                                                         28 GVLLVLGLLINSLALWVFCCRMOOWTETRIYMTNLAVADLCLLCTL-PFVLHSLRD---T
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                                                                                                          Gape
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                                                                                                       37;
                                                   Length 254;
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                                                 20.4%; Score 329.5; DB 6; Length 2:
33.7%; Pred. No. 9.5e-25;
iive 54; Mismatches 88; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Regulation of Human CysiT2-Like GPCR
TITLE OF INVENTION: Regulation of Human CysiT2-Like GPCR
TITLE OF INVENTION: Protein
FILE REPERENCE: 04974.00458
CURRENT APPLICATION NUMBER: US/11/157,930
CURRENT PELLING DATE: 2005-06-22
PRIOR FILING DATE: 2005-06-22
PRIOR FILING DATE: 2000-04-09
PRIOR PILING DATE: 2000-04-07
PRIOR PILING DATE: 2000-04-07
PRIOR RILING DATE: 2000-12-13
NUMBER OF SEQ. ID NOS: 16
NUMBER OF SEQ. ID NOS: 16
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Best Local Similarity 28.4%; Pred. No. 2.4e-23;
Matches 89; Conservative 64; Mismatches 139; Indels
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Publication No. US20050266482A1
GENERAL INFORMATION:
                                                                                                     91; Conservative
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TYPE: PRT
ORGANISM: Homo sapiens
                                                                       Best Local Similarity
Matches 91; Conserv
JS-10-877-346-83
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US-11-157-930-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    165 STRHN------FINSMRFPLLGFYLPLAVVVFCSLKVVTALAQRPPTDVGQA 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         210 BATRKAKRMVWANLLVFVVCFLPLHVGLTV----RLAVGWNACALLETIRRALYITSKLS 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             263 QTERRATVLVVLLPIPICWLPFQISTFLDTLHRLGI-LSSCQDERIIDVITQIASFMA 321
                                                                                                                                                                                                                                                                                                           53 TETRIYMTNLAVADLCLLCTLPFVLHSLRDTSD----TPLCQLSQGIYLTNRYMSISLVT 108
                                                                                                                                                                                                                                                                                                                                                                               AIAVDRYVAVRHPLRARGLRSPRQAAAVCAVLW--VLVIGS--LVARWLLGIQEGGFCFR 164
                                                                                                                                                                                                                                         1 MNGTYNTCGSSDLTW-----PPAIKLGFYAYLGVLLVIGLLLNSLALWVFCCRMQQW 52
                                                                                                                                                                                                                                                                         38 INGTFAQSKCPQVEWIGWINTIQPP-----FLWVIPVIATIENIFVLSVFCLHKSSC 89
                                                                                                                                                                                                        51;
                                                                                                                                                                        Length 391;
                                                                                                                                                                      19.3%; Score 311.5; DB 7; Length 3 llarity 27.6%; Pred. No. 8.3e-23; Conservative 54; Mismatches 128; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 322 YSNSCLNPLVYVIVGKRFRKKS 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              266 DANCCLDAICYYYMAKEFQRAS 287
PRIOR APPLICATION NUMBER: 60/603,948
PRIOR FILING DATE: 2004-08-24
NUMBER OF SEQ ID NOS: 590
SOFTWARE: PatentIn version 3.3
SEQ ID NO 52
LENGTH: 391
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Publication No. US20050288241A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: DeCitatofaro, Marc
APPLICANT: Padigaru, Muralidhara
APPLICANT: Miller, Charles
APPLICANT: Tchernev, Velizar
APPLICANT: Zhong, Mei
APPLICANT: Anderson, David
APPLICANT: Ballinger, Robert
APPLICANT: Syrek, Kimberly
APPLICANT: Ratelli, Luca
APPLICANT: Ratelli, Luca
APPLICANT: Retelli, Luca
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Taupier Jr., Raymond
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Mezes, Peter
Patturajan, Meera
Burgess, Cahterine
Risen, Andrew
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Gusev, Vladimir
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Zerhusen, Bryan
Andrew, David
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                                                                                                                    ORGANISM: Homo sapiens
US-11-127-877-52
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Best Local Similarity
Matches 89; Conserv
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Boldog,
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86 ----TPLCQLSQGIYLTNRYMSISLVTAIAVDRYVAVRHPLRARGIR-SPRQAAAVCAVL 140
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CURRENT APPLICATION NUMBER: US/10/055,877
CURRENT APPLICATION NUMBER: US/10/055,877
CURRENT APPLICATION NUMBER: US/10/055,877
FRIOR PILING DATE: 2001-01-29
PRIOR PLING DATE: 2001-01-19
PRIOR PLING DATE: 2001-01-24
PRIOR PLING DATE: 2001-01-25
PRIOR APPLICATION NUMBER: 60/264,137
PRIOR PLING DATE: 2001-01-25
PRIOR PLING DATE: 2001-01-26
PRIOR PLING DATE: 2001-01-26
PRIOR PLING DATE: 2001-01-26
PRIOR PLING DATE: 2001-01-36
PRIOR PLING DATE: 2001-01-36
PRIOR PLING DATE: 2001-01-36
PRIOR PLING DATE: 2001-01-36
PRIOR PLING DATE: 2001-01-34
PRIOR PLING DATE: 2001-03-14
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IIILE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoded Thereby
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Miller, Charles
Tohernev, Velizar
Zhong, Mei
Anderson, David
Ballinger, Robert
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APPLICANT: Padigaru, Muralidha
APPLICANT: Miller, Charles
APPLICANT: Tchernev, Velizar
APPLICANT: Zhong, Mei
APPLICANT: Ballinger, Robert
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ORGANISM: Artificial Sequence
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Best Local Similarity 32.00
Best Local Similarity
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SEQ ID NO 225
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US-10-055-877-237
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GFYLPLAVVVFCSLKVVTALAQRPPTDVGQABATRKAKRNVWANLLVFVVCFLPLHVGL- 237
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ORGANISM: Homo sapiens
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Matches 88; Conserva
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APPLICANT: Boldog, Ference

TITLE OF INVENTION: Novel Polypeptides and Mucleic Acids Encoded Thereby
FILE REPERENCE: 21402-251

CURRENT PAPLICATION NUMBER: US/10/055,877

CURRENT FILING DATE: 2002-01-22

PRIOR PILING DATE: 2001-01-9

PRIOR PILING DATE: 2001-01-9

PRIOR PILING DATE: 2001-01-24

PRIOR PILING DATE: 2001-01-24

PRIOR PILING DATE: 2001-01-25

PRIOR PILING DATE: 2001-01-25

PRIOR PILING DATE: 2001-01-25

PRIOR PILING DATE: 2001-01-25

PRIOR PILING DATE: 2001-01-26

PRIOR PILING DATE: 2001-01-26

PRIOR PILING DATE: 2001-01-26

PRIOR PILING DATE: 2001-01-26

PRIOR PILING DATE: 2001-01-36

PRIOR PILING DATE: 2001-01-36

PRIOR PILING DATE: 2001-01-30

PRIOR PILING DATE: 2001-01-30

PRIOR PILING DATE: 2001-03-02

PRIOR PILING DATE: 2001-03-04

PRIOR PILING DATE: 2001-03-04

PRIOR PILING DATE: 2001-03-14

PRIOR PILING DATE: 2001-03-14

PRIOR PILING DATE: 2001-03-14
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18.6%; Score 300; DB 6; Length 259;
Best Local Similarity 32.6%; Pred. No. 6.8e-22;
Matches 92; Conservative 49; Mismatches 85; Indels 56; Gaps
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US-10-055-877-237
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Taupier Jr., Raymond
Pena, Carol
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Burgess, Cahterine
Eisen, Andrew
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Shimkets, Richard
Gusev, Vladimir
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Gerlach, Valerie
Spytek, Kimberly
Ratelli, Luca
Kekuda, Ramesh
                                                                         Guo, Xiaojia
Zerhusen, Bryan
Andrew, David
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LENGTH: 259
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75 VADLSCVLVLPTRLVYHFSGNHWPFGEIACRLTGFLFYLNMYASIYFLTCISADRFLAIV 134
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Sequence 4, Application US/11157930

Publication No. US20050266482A1

GENERAL INFORMATION:
APPLICANT: Xiao, Yonghong

TITLE OF INVENTION: Regulation of Human CysLT2-Like GPCR
TITLE OF INVENTION: Protein
FILE REFERENCE: 04974.00458

CURRENT APPLICATION NUMBER: US/11/157,930

CURRENT FILING DATE: 2005-06-22

PRIOR APPLICATION NUMBER: G/195,196

PRIOR APPLICATION NUMBER: 60/195,196

PRIOR APPLICATION NUMBER: 60/195,196

PRIOR PILING DATE: 2000-04-07

PRIOR PILING DATE: 2000-01-07

PRIOR PILING DATE: 2000-01-07

SROID NO 4.0

SOFTWARE: FastSEQ for Windows Version 4.0

LENGTH-1330
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                                                                                                                     218 LDTLCLSIIMSSTCELERVLPTALLVTLWLAYVNSCLNPIIY 259
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Sequence 6, Application US/11157930

Publication No. US2005026482A1

GENERAL INFORMATION:

APPLICANT: Xiao, Yonghong

TITLE OF INVENTION: Regulation of Human CyaLT2-Like GPCR

TITLE OF INVENTION:

FILE REFERENCE: 04974.00458
                                                                                  238 -- TVRLAVGWNA-CALLETIRRALYITSKLSDANCCLDAICY
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61; Gaps

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89; Conservative
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US-11-127-877-46
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Sequence 66, Application US/11127877

Publication No. US20050287565A1

GENERAL INFORMATION:

APPLICANT: Merchiere, Pascal G.

APPLICANT: Spitraels, Koenraad F. F.

APPLICANT: Laenen, Wendy

TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting

TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting

TITLE OF INVENTION: Methods, Logic Beta Protein Production

FILE REFERENCE: P27, 800-B USA

CURRENT APPLICATION NUMBER: US/11/127,877

CURRENT APPLICATION NUMBER: 60/570,352

PRIOR PILING DATE: 2004-05-12

PRIOR FILING DATE: 2004-06-12

PRIOR FILING DATE: 2004-08-24

NUMBER OF SEQ ID NOS: 590

SOUTHARE PATENTIN VERSION 3.3
                                                                                                                                                                                                                                                                                                                                                             64 VADLCLLCTLPFVLHSLRDTSDTPL----CQLSQGIYLTNRYMSISLVTAIAVDRYVAVR 119
                                                                                                                                                                                                                                                                                                                                                                                                                            |||| : || || : || || : || 103 VADISCVLVLPTRLVYHPSGNHWPFGEIACRLTGFLFYLMMYASIYPLTCISADRFLAIV 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           120 HPLRARGLRSPROAAAVCAVLWVLVIGS----LVARWLLGIQEGGFCF----RSTRHNF 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  171 NSMRPPLLGFYLPLAVVVFCSLKVVTALAQRPPTDVG---QAEATRKAKRMVWANLLVFV 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   228 VCFLPLHVGLTV---RLAVGWNACALLETIRRALYITSKLSDANCCLDAICYYYMAKEFQ 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 TYNTCGSSDLTWPPAIKLGFYAYLGVLLVLGLLLNSLALWVFCCRMQQWTETRIYMTNLA 63
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                                                                                                                                                                                                                                                                       18.5%; Score 298; DB 7; Length 367; 29.1%; Pred. No. 1.6e-21;
                                                                                                                                                                                                                                                                                                            54; Mismatches 128; Indels
 CURRENT APPLICATION NUMBER: US/11/157,930
CURRENT FILING DATE: 2005-06-22
PRIOR APPLICATION NUMBER: US/09/828,478
PRIOR APPLICATION NUMBER: 60/195,196
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: 60/195,196
PRIOR FILING DATE: 2000-01-07
PRIOR FILING DATE: 2000-01-07
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FASESEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                          Query Match 18.5
Best Local Similarity 29.1
Matches 88, Conservative
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                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Homo sapiens
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Best Local Similarity
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US-11-127-877-66
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LENGTH: 358
                                                                                                                                                                                          LENGTH: 367
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Sequence 46, Application US/11127877

Sequence 46, Application WS/11127877

Publication No. US20050287565A1

GENERAL INFORMATION:
APPLICANT: Merchiers, Pascal G.
APPLICANT: Apficable, Koenraad F. F.
TITLE OF INVENTION: Amyloid-Beta Protein Production
FILLE REPERENCE: P27,800-B USA
FILLE REPERENCE: P27,800-B USA
CURRENT APPLICATION NUMBER: US/11/127,877

CURRENT FILING DATE: 2005-05-12
PRIOR PILING DATE: 2004-05-12
PRIOR PILING DATE: 2004-05-12
PRIOR PILING DATE: 2004-06-12

PRIOR PILING DATE: 2004-08-14

NUMBER OF SEQ ID NOS: 590

SOFTWARE: PatentIn version 3.3

SEQ ID NO 46 section 3.3
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                                                                                                                                                                                                                                                                                                                                                                                                                           CR-----VFALTVLEFILIPLLVISVFTGRIMCALSR--PGLLHQGRQRRVRAMQLLLT 245
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                                                                                                                                                                                                                                                                           SISLVTAIAVDRYVAVRHPLRARGLRSPRQAAAVCAVLWVLVIGSLVARWLLGIQEGGFC 162
                                                                                                                                                                                                                                                                                                           163 FRSTRHNFNSMRFPLLGFYLPLAVVVFCSLKVVTALAQRPPTDVGQAEATR-KAKRMVWA 221
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          246 VLIIFLVCFTPFHAR---QVAVALWPDMPHHTSLVVYHVAVTLSSLNSCMDPIVYCFVTS 302
                                                                                                                                                           61 NLAVADL-------CLLCTLPFVLHSLRDTSDTPLCQLSQGIYLTNRYM 102
                                                                                                                                                                                                                   94 NLVVTDLLVGLSLPTRFAVYYGARGCLRCAFPHVLG--------YFLNMHC 136
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                                                                         45 LHGTF------PGLCVALMAVHGAIFLAGLVLNGLALYVFCGRTRAKTPSVIXTI 93
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                                                 1 MNGTYNTCGSSDLTWPPAIKLGFYAYLGVLLVLGLLLNSLALMVFCCRMQQWTBTRIYMT
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42; Mismatches 111; Indels
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18.4%; Score 296.5; DB 7;
Best Local Similarity 26.2%; Pred. No. 2.2e-21;
Matches 88; Conservative 72; Mismatches 137;
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Publication No. US2005027205431
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REPERENCE: CLO01559
CURRENT RELIGING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 523
KAKRMVWANLLVFVVCFLPLHVGLTVRLAVGWN-----ACALLETIRRALYITSKLSDAN 268
                               |: :| | | | | | : | | | : | 3.57 KSIYLVIIVLTVFAVSYIPFHVMKTMNLRARLDFQTPAMCAFNDRVYATYQVTRGLASLN 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        75 FVLHSLRDTSD--TPLCQLSQGIYLTNRYMSISLVTAIAVDRYVAVRHPLRARGLRSPRQ 132
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Publication No. US2005026055A1
GENERAL INFORMATION:
APPLICANT: Gray, Patrick W.
Schweickart, Vicky L.
Raport, Carol J.
TITLE OF INVENTION: Chemokine Receptor Materials and Methods
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 17.7%; Score 286.5; DB 6; Length 352; Best Local Similarity 26.2%; Pred. No. 1.9e-20; Matches 75; Conservative 62; Mismatches 118; Indels 31;
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STREET: 6300 Sears Tower, 233 S. Wacker Drive
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                                                                                                   269 CCLDAICYYMAKEFQEASALAVAPRAKAHKSQDSL 304
                                                                                                                             317 SCVDPILYFLAGDTFRR--RLSRATRKASRRSEANL 350
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MEDIUM TYPE: Floppy disk
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STATE: Illinois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Homo sapiens
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US-11-068-686-2
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75 FVLHSLRDTSD--TPLCQLSQGIYLTNRYMSISLVTAIAVDRYVAVRHPLRARGLRSPRQ 132
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26.2%; Pred. No. 1.9e-20;
tive 62; Mismatches 118; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc feature
OTHER INFORMATION: /= "88C amino acid sequence"
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                    APPLICATION NUMBER: US/11/068,686
FILING DATE: 28-Feb-2005
CLASSIFICATION NUMBER: US/11/068,686
ATTORNEY/AGENT INFORMATION:
NAME: Noland, Greta E.
REGISTRATION NUMBER: 35,302
REPERENCE/DOCKET NUMBER: 27866/33670
TELECOWNUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 352 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 26.2 les 75, Conservative
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Sequence 20, Appl
Sequence 492, App
Sequence 84, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 176, Appl
Sequence 176, Appl
Sequence 116, Appl
Sequence 116, Appl
Sequence 117, Appl
                                                                              ; Search time 118.5 Seconds (without alignments)
1089.530 Million cell updates/sec
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1614
1 MNGTYNTCGSSDLTWPPAIK......AVAPRAKAHKSQDSLCVTLA 309
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Sequence
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1: /cgn2_6/ptodata/1/pubpāa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*
GenCore version 5.1.7
(c) 1993 - 2006 Biocceleration Ltd
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US-10-225-567A-492

US-10-505-486-84

US-10-505-486-84

US-10-157-031-351

US-10-091-821B-11

US-10-091-821B-11

US-10-225-567A-225

US-10-225-567A-225

US-10-225-38A-176

US-10-268-332-11

US-10-75-365-11

US-10-75-365-11

US-10-75-365-11

US-10-75-366-114

US-10-75-366-114

US-10-75-366-114

US-10-268-332-10

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US-10-268-332-10
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US-10-897-815-159
US-10-930-662-159
US-09-930-334-16
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                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                             1867569 seqs, 417829326 residues
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                                                                                                                                                                                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                    9, 2006, 01:16:44
                                                        protein search, using sw model
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seq length: 200000000
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Match Length DB
               Copyright
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Perfect score:
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Maximum DB
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Sequence 54202, A Sequence 54202, A Sequence 36, Appl Sequence 226, Appl Sequence 36, Appl Sequence 36, Appl Sequence 36, Appl Sequence 36, Appl Sequence 4, Appl Sequence 4, Appl Sequence 766, Appl Sequence 2, Appl Sequence 2, Appl Sequence 12, Appl Sequence 12, Appl Sequence 12, Appl
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Sequence 20, Application US/09768877

Patent No. US20020150896A1

GENERAL INFORMATION:

APPLICANT: POLONSKY, KENNETH S.

APPLICANT: HORIKAWA, YUKIO

APPLICANT: COX, NANCY J.

APPLICANT: COX, NANCY J.

APPLICANT: SHEDNA, SEAMUS

APPLICANT: COXN, NANCY J.

APPLICANT: COXNI, KENICHI

APPLICANT: CHANI, KENICHI

APPLICANT: CHANI, KENICHI

APPLICANT: HANIS, CRAIG L.

APPLICANT: BELL, GRAEME I.

TITLE OF INVENTION: METHODS OF TREATMENT OF TYPE 2 DIABETES

FILE REFERENCE: ARCD: 307

CURRENT APPLICATION NUMBER: 09/422,869

PRIOR FILING DATE: 1999-10-21

NUMBER OF SEQ ID NOS: 30

SOFTWARE PATENTIN VET. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 309;
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100.0%; Pred. No. 1.2e-145;
ive 0; Mismatches 0;
         US-10-167-192-1
US-10-400-991-4
US-10-450-763-54202
US-10-505-486-45
US-10-321-807-36
US-10-292-027-26
US-10-292-798-668
US-10-314-048A-36
US-10-314-048A-36
US-10-997-652-36
US-10-997-652-36
US-10-90-622-36
US-10-910-622-36
US-10-910-622-36
US-10-910-623-36
US-10-910-622-36
US-10-910-622-36
US-10-910-622-36
US-10-110-1161-766
US-10-017-161-106
US-10-017-161-106
US-10-017-161-106
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Matches 309; Conservative
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; Pred. No. 1.2e-145;
0; Mismatches 0;
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Publication No. US20050118639A1

GENERAL INFORMATION:

APPLICANT: Takeda Chemical Industries, Ltd.

TITLE OF INVENTION: Determination of a ligand
FILE REFERENCE: P03-0006PCT US/10/505,486

CURRENT APPLICATION NUMBER: US/10/505,486

PRIOR APPLICATION NUMBER: US 2002-45728

PRIOR FILING DATE: 2002-02-22

PRIOR FILING DATE: 2002-07-23

PRIOR FILING DATE: 2002-07-23

PRIOR PLICATION NUMBER: UP 2002-298237

PRIOR PLICATION NUMBER: UP 2002-298237

NUMBER OF SEQ ID NOS: 233

LENGTH: 547
                                                                                                                                                                                         100.0%;
NUMBER OF SEQ ID NOS: 3114
SOFTWARE: Patentin version 3.1
SEQ ID NO 44
LENGTH: 309
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Best Local Similarity 100.0
Matches 309; Conservative
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Matches 308; Conservative
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                                                                                            TYPE: PRT
ORGANISM: homo sapiens
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ORGANISM: Human
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US-10-505-486-84
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                                                                                                                                                                                              Sequence 492, Application US/10225567A
| Publication No. US20030113798A1
| Publication No. US20030113798A1
| Publication No. US20030113798A1
| GENERAL INFORMATION:
| APPLICANT: LifeSpan Biosciences | APPLICANT: Burmer, Glenna C. | APPLICANT: Burmer, Glenna C. | APPLICANT: Roush, Christine Court of Christine C. | APPLICANT: Roush, Christine C. | APPLICANT: Patentin version 3.1
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Publication No. US20050037439A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Pharmacia Corporation
APPLICANT: Bourner, Maureen J.
TITLE OF INVENTION: DIFFRENTIALLY EXPRESSED GENES INVOLVED IN CANCER, THE
TITLE OF INVENTION: POLYPEPTIDES ENCODED THEREBY, AND METHODS OF USING THE SAME;
FILE REPERENCE: 01046/1
CURRENT APPLICATION NUMBER: US/10/696,639
CURRENT PILING DATE: 2003-10-29
PRIOR PILING DATE: 2003-10-29
241 LAVGWNACALLETIRRALYITSKLSDANCCLDAICYYYMAKEFQEASALAVAPRAKAHKS 300
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100.0%; Score 1614; DB 4; Length 309;
Best Local Similarity 100.0%; Pred. No. 1.2e-145;
Matches 309; Conservative 0; Mismatches 0; Indels 0
                                              ODSLCVTLA 309
                                                                                     301 ODSLCVTLA 309
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US-10-696-639-44
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LENGTH: 309
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Sequence 44, Application US/10081810
Sequence 44. Application US/10081810
Publication No. US20030064438A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL SQUIDE COMPANY
TITLE OF INVENTION: USES THEREOF
FILE OF INVENTION: USES THEREOF
FILE REFERENCE:
FURENT APPLICATION NUMBER: US/10/081,810
CURRENT APPLICATION NUMBER: US 60/270,793
PRIOR APPLICATION NUMBER: US 60/270,793
PRIOR APPLICATION NUMBER: US 60/270,792
PRIOR APPLICATION NUMBER: US 60/296,427
                                        APPLICANT: HAWKEN, D.R.
APPLICANT: CACACE, A. R.
APPLICANT: GACACE, A. R.
APPLICANT: CACACE, A. R.
APPLICANT: CACACE, M. G.
ITILE OF INVENTION: EXPRESSED HIGHLY IN IMMUNE- AND COLON- RELATED TISSUES FILE REPERRACE: D0042NP
CURRENT FILING DATE: 2002-06-10
PRIOR FILING DATE: 2000-09-27
PRIOR FILING DATE: 2001-01-17
PRIOR PLICATION NUMBER: 60/235,713
PRIOR FILING DATE: 2001-01-17
PRIOR PLICATION NUMBER: 60/235,713
PRIOR FILING DATE: 2001-01-17
PRIOR PLICATION NUMBER: 60/335,085
PRIOR FILING DATE: 2001-07-13
PRIOR FILING DATE: 2001-07-13
PRIOR PLICATION NUMBER: 60/313,171
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24.9%; Score 402; DB 3; Length 370.
Best Local Similarity 34.1%; Pred. No. 8.2e-30;
Matches 103; Conservative 60; Mismatches 111; Indels
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                        RAMANATHAN, C
HAWKEN, D.R.
CACACE, A.
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US-09-964-821B-11
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APPLICANT: Yankovsky, N. K.
APPLICANT: Yankovsky, N. K.
APPLICANT: Yankovsky, N. K.
APPLICANT: Lobashev, A. V.
APPLICANT: Lobashev, A. V.
APPLICANT: Lobashev, L. L.
TITLE OF INVENTION: In silico screening for phenotype-associated expressed sequences TITLE OF INVENTION: 10 silico screening for phenotype-associated expressed sequences CURRENT FILING DATE: 2002-05-30
CURRENT FILING DATE: 2002-05-30
NUMBER OF SEQ ID NOS: 415
SEQ ID NO 35:
LENGTH: 309
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                                                                                                            241 LAVGWNACALLETIRRALYITSKLSDANCCLDAICYYYMAKEFQEASALAVAPRAKAHKS 300
241 LAVGWNACALLETIRRALYITSKLSDANCCLDAICYYYMAKEFQEASALAVAPRAKAHKS 300
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YLPLAVVVPCSLKVVTALAQRPPTDVGQABATRKAARMVWANLLVFVVCFLPLHVGLTVR
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99.4%; Pred. No. 1.6e-144;
live 0; Mismatches 2;
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US-09-964-821B-11
; Sequence 11, Application US/09964821B
; Publication No. US20030186360A1
; GENERAL INFORMATION:
; APPLICANT: FEDER, J. N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 351, Application US/10157031
Publication No. US20030108890A1
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; ORGANIȘM: Homo sapiens
US-10-157-031-351
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223 CSSVVLRTL--RKPATLSQIGTNKKVLKMITVHMAVFVVCFVPYNSVLFLYALVRSQAI 280
                                                                                                                                                                249 --ALLETIRRALY-ITSKLSDANCCLDAICYYYMAKEFQEASALAVAFRAKAHKSQDSLC 305
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281 INCFLERFAKIMYPITLCLATLNCCFDPFIYYFTLESFQKSFYI-----NAHIRMESLF 334
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                                                                      190 CSLKVVTALAQRPPTDVGQAEAT-RKAARMVWANLLVFVVCFLPLHVGLTVRLAVGWNAC 248
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Best Local Similarity 34.1%; Pred. No. 8.2e-30;
Matches 103; Conservative 60; Mismatches 111; Indels
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CURRENT PELICATION NUMBER: US/10/024,298A

CURRENT FILING DATE: 2003-04-08

PRIOR PELING DATE: 2003-04-08

PRIOR PILING DATE: 2001-08-24

PRIOR PILING DATE: 2001-03-26

PRIOR PILING DATE: 2001-03-26

PRIOR PILING DATE: 2000-12-28

PRIOR PILING DATE: 2000-12-28

PRIOR PILING DATE: 2000-12-28

PRIOR PILING DATE: 2001-03-26

PRIOR PILING DATE: 2001-03-26

PRIOR APPLICATION NUMBER: JPD088912/2001

PRIOR PILING DATE: 2001-03-26

PRIOR PILING DATE: 2001-03-26

PRIOR PILING DATE: 2001-03-26

PRIOR PILING DATE: 2001-03-26

PRIOR PILING DATE: 2001-12-28

NUMBER OF SEQ ID NOS: 182
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APPLICANT: AKIO MATSUDA
APPLICANT: Goichi HONDA
APPLICANT: Bhuji MURAMATSU
APPLICANT: Yukiko NGANO
TITLE OP INVENTION: NF-K B Activating Gene
FILE REPERENCE: 1254-0191P
                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 176, Application US/10024298A
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SEQ ID NO 176
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US-10-024-298A-176
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US-10-024-298A-176
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APPLICANT: Brown, Joseph P.
APPLICANT: Brown, Joseph P.
APPLICANT: Bruner, Glenna C.
TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS FILE REFERENCE: 1920-4-4
CURRENT APPLICATION NUMBER: US/10/225,567A
PRIOR PILING DATE: 2001-12-19
PRIOR PILING DATE: 2000-12-19
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104 WPFGDT-LCKISGTAFLTNIYGSMLFLTCISVDRPLAIVYPFRSRTIRTRRNSAIVCAGV 162
                                                                                                                                                                                                                                                                                                            44 AVYSVVFILGLITINSVSLFVFCFRAMOMSSTAIFITMLAVSDLLFVCTLPFKIFYNFNRH 103
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                                                                                                                                                                                                                                                                                  25 AYLGVLLVLGLLLNSLALWVFCCRMQQWTETRIYMTNLAVADLCLLCTLPF-VLHSLR--
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                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                   Query Match

24.9%; Score 402; DB 4; Length 370;

Best Local Similarity 34.1%; Pred. No. 8.2e-30;

Matches 103; Conservative 60; Mismatches 111; Indels 28;
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, Publication ND. US20030113798A1
, GENERAL INFORMATION:
NUMBER OF SEQ ID NOS: 58
SOFTWARE: Patentin version 3.0
SEQ ID NO 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 2292
SOPTWARE: Patentin version 3.1
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Best Local Similarity 34.1%
Matches 103, Conservative
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US-10-225-567A-225
                                                                                       TYPE: PRT
ORGANISM: Homo sapiens
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US-10-225-567A-225
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82 -DISDIBLOQLSQCIYLINRYMSISLVTALAVDRYVAVRHPLRARGLRSPRQAAAVCAVL 140
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TITLE OF INVENTION: NF-KB ACTIVATING GENE FILE REPERENCE: 1254-0229P
CURRENT APPLICATION NUMBER: UP 2000-40228B
FRIOR APPLICATION NUMBER: UP 2000-40228B
FRIOR FILING DATE: 2000-12-28
FRIOR FILING DATE: 2001-03-26
FRIOR APPLICATION NUMBER: UP 2001-054018
FRIOR FILING DATE: 2001-03-26
FRIOR APPLICATION NUMBER: US 60/254018
FRIOR FILING DATE: 2001-03-24
FRIOR FILING DATE: 2001-12-28
FRIOR FILING DATE: 2001-12-28
FRIOR FILING DATE: 2001-13-26
FRIOR FILING DATE: 2001-13-28
FRIOR FILING DATE: 2001-03-26
FRIOR FILING DATE: 2001-03-24
              CURRENT PERFICATION NUMBER: US/10/268,332
CURRENT PILING DATE: 2002-10-10
PRIOR PILING DATE: 2000-09-27
PRIOR FILING DATE: 2000-09-27
PRIOR FILING DATE: 2001-01-16
PRIOR PILING DATE: 2001-01-16
PRIOR PILING DATE: 2001-07-13
PRIOR PILING DATE: 2001-08-17
PRIOR PILING DATE: 2001-09-26
NUMBER: OF SEQ ID NOS: 66
SOFTWARE: PATENTIN VETSION 3.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 103; Conservative
FILE REFERENCE: D0042A CIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Homo sapiens
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Publication No. US20030175748A1
GENERAL INFORMATION:
APPLICANT: Briston-Myers Squibb Company
TITLE OF INVENTION: NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPRBMY3, EXPRESSED HIGHI
TITLE OF INVENTION: NOVEL HUMAN G-PROTEIN COUPLED TISSUES
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24.9%; Score 402; DB 4; Length 37<sup>n</sup>
Best Local Similarity 34.1%; Pred. No. 8.2e-30;
Matches 103; Conservative 60; Mismatches 111; Indels
                                                                                                                                                                                                                                                                                             TITLE OF INVENTION, WERB Activating Generative Courrent Marsuna, MFRB Activating General Englement 124-0192P

FILE REFERENCE: 1254-0192P

CURRENT APPLICATION NUMBER: US/10/042,211A

CURRENT FILING DATE: 2002-01-11

PRIOR PRILING DATE: 2000-12-2B

PRIOR FILING DATE: 2001-03-26

PRIOR PLING DATE: 2001-03-26

PRIOR PLING DATE: 2001-03-26

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PRIOR PLING DATE: 2001-03-26

PRIOR FILING DATE: 2001-03-26

PRIOR FILING DATE: 2001-03-26

PRIOR FILING DATE: 2001-03-26

PRIOR FILING DATE: 2001-08-24

NUMBER OF SEQ ID NOS: 182

SEQ ID NO 176
                                                                                                                                                                                             US-10-042-211A-176
; Sequence 176, Application US/10042211A
; Publication No. US20030170719A1
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CORGANISM: Homo sapiens
US-10-042-211A-176
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US-10-268-332-11
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     CSLKVVTALAQRPPTDVGQAEAT-RKAARMVWANLLVFVVCFLPLHVGLTVRLAVGWNAC 248
                                 249 --ALLETIRRALY-ITSKLSDANCCLDAICYYYMAKEFQEASALAVAPRAKAHKSQDSLC 305
                                                                                                                                281 TNCFLERPAXIMYPITLCLATINCCFDPFIYYFTLESFQKSFYI-----NAHIRMESLF 334
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24.9%; Score 402; DB 4; Length 37
Best Local Similarity 34.1%; Pred. No. 8.2e-30;
Matches 103; Conservative 60; Mismatches 111; Indels
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APPLICANT: Shuji MURAMATEU
APPLICANT: Shuji MURAMATEU
TITLE OF INVENTION: NP-K B Activating Gene
FILE REPERENCE: 1254-0191P
CURRENT APPLICATION NUMBER: US/10/024,298A
CURRENT FILING DATE: 2003-04-08
PRIOR APPLICATION NUMBER: 60/214,385
PRIOR APPLICATION NUMBER: 60/214,385
PRIOR FILING DATE: 2001-03-26
PRIOR FILING DATE: 2001-03-26
PRIOR FILING DATE: 2000-12-28
PRIOR FILING DATE: 2000-12-28
PRIOR FILING DATE: 2001-03-26
PRIOR FILING DATE: 2001-03-26
PRIOR FILING DATE: 2001-03-26
PRIOR PLING DATE: 2001-03-26
PRIOR PLING DATE: 2001-03-26
PRIOR FILING DATE: 2000-12-28
NUMBER: OF SEQ ID NOS: 182
SEQ ID NO 176
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APPLICANT: Akio MATSUDA
                                                                                                                                                                                                                                                                                                                                                                          Sequence 176, Application US/10024298A Publication No. US20040214167A9 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Goichi HONDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Homo sapiens
US-10-024-298A-176
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                                                                                                                                                                                                                                                                              25 AYLGYLLVLGLLLNSLALWVFCCRMQQWTETRIYMTNLAVADLCLLCTLPF-VLHSLR-- 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-775-965-11

Sequence 11, Application US/10775965

Publication No. US20040209808A1

GENERAL INFORMATION:

APPLICANT: Bristol-Myers Squibb Company

APPLICANT: Kornacker, Michael

TITLE OF INVENTION: MODULATORS OF HUMAN G-PROTEIN COUPLED RECEPTORS

FILE REFERENCE: D0.286 NP

CURRENT PELING DATE: 2004-02-10

PRIOR PILNG DATE: 2004-02-10

PRIOR PILNG DATE: 2003-02-11

NUMBER OF SEQ ID NOS: 112

SOPTWARE: Patentin version 3.2
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                                                                                                                                                                            Query Match
24.9%; Score 402; DB 4; Length 370;
Best Local Similarity 34.1%; Pred. No. 8.2e-30;
Matches 103; Conservative 60; Mismatches 111; Indels
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24.9%; Score 402; DB 4; Length 370;
Best Local Similarity 34.1%; Pred. No. 8.2e-30;
Matches 103; Conservative 60; Mismatches 111; Indels
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 176
LENGTH: 370
                                                                                                 ; ORGANISM: Homo sapiens
US-10-617-217A-176
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ORGANISM: Homo sapiens
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LENGTH: 370
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                                                                               TYPE: PRT
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APPLICANT: Healy. Atleen.
APPLICANT: Galvin, Katherine M.
APPLICANT: Tomlinson, James E.
APPLICANT: TITLE OF INVENTION: 1466, 12282, 6356, 1649, 6555, 1010, 2164, 17662, 1771, 1771, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 1774, 
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Best.Local Similarity 34.1%; Pred. No. 8.2e-30;
Matches 103; Conservative 60; Mismatches 111; Indels 28; Gaps
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NUMBER OF SEQ ID NOS: 130
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 86
LENGTH: 370
                                                                                                                                                                                                                                                                        APPLICANT: Millennium Pharmaceuticals, Inc.
                                                                                                                                                               Sequence 86, Application US/10753267
Publication No. US20050037946A1
                                                                                                                                                                                                                                                                                                     Stagliano, Nancy E.
Healy, Aileen
Acton, Susan L.
Galvin, Katherine M.
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CRGANISM: Homo Sapiens
US-10-753-267-86
                                                                                                                                                                                                                                       GENERAL INFORMATION
KT 336
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1. /cgn2_6/ptodata/1/pubpaa/US06_NEW_FUB.pep:*
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Maximum Match 100%
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### STIMMARIE

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|---------------|-------|-------|--------|----|-------------------|-------------------|
| Result<br>No. | Score | Query | Length | DB | ΙD                | Description       |
| -             | 334.5 | 20.7  | 254    | 9  | US-10-055-877-248 | Sequence 248, App |
| 8             | 334.5 | 20.7  | 254    | 9  | US-10-055-877-327 | Sequence 327, App |
| m             | 334.5 | 20.7  | 254    | 9  | US-10-055-877-340 |                   |
| 4             | 334.5 | 20.7  | 254    | 9  | US-10-877-346-83  | 83, 7             |
| S             | 317.5 | 19.7  | 346    | 7  | US-11-157-930-2   | 2, 2              |
| 9             | 315.5 | 19.5  | 365    | 9  | US-10-995-561-545 | 545,              |
| 7             | 312.5 | 19.4  | 391    | 7  |                   | 52, 7             |
| 8             | . 305 | 18.9  | 259    | 9  | US-10-055-877-225 | Sequence 225, App |
| ٥             | 305   | 18.9  | 259    | 9  | US-10-055-877-237 | 237,              |
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| 12            | 298.5 | 18.5  | 373    | 7  | US-11-127-877-46  | 46,               |
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| 14            | 288.5 | 17.9  | 352    | 9  |                   | 22                |
| 15            | 288.5 | 17.9  | 352    | 7  | US-11-068-686-2   | Sequence 2, Appli |
| 16            | 288.5 | 17.9  | 352    | 7  | US-11-127-877-61  | 61                |
| 17            | 287.5 | 17.8  | 352    | 7  | US-11-068-686-20  | 20                |
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| 21            | 255.5 | 15.8  | 359    | 9  | US-10-995-561-712 | 712               |
| 22            | 255.5 | 15.8  | 359    | 9  | US-10-995-561-716 | 716,              |
| 23            | 255.5 | 15.8  | 359    | 9  | US-10-876-787-2   | 'n                |
| 24            | 255.5 | 15.8  | 359    | 7  | US-11-127-877-65  | 65,               |
| 25            | 255.5 | 15.8  | 388    | 9  | US-10-995-561-713 | Sequence 713, App |

| Sequence 714, App Sequence 715, App Sequence 55, Appl Sequence 2, Appli Sequence 818, App Sequence 817, App Sequence 60, Appl Sequence 64, Appli Sequence 4, Appli Sequence 64, Appli Sequence 636, Appli Sequence 637, App Sequence 637, App Sequence 637, Appli Sequence 64, Appli Sequence 64, Appli Sequence 637, Appli Sequence 637, Appli Sequence 64, | Sequence 59, Appl<br>Sequence 32, Appl |
|--|--|
| US-10-995-561-714 US-11-21-877-55 US-11-127-877-55 US-10-995-561-838 US-10-995-561-838 US-10-995-561-837 US-10-995-561-837 US-11-127-877-60 US-11-127-877-60 US-11-127-877-60 US-11-27-877-60 US-11-27-877-60 US-11-27-877-60 US-11-218-281-28 US-11-218-281-12 US-11-218-281-12 US-11-218-281-24 US-11-218-281-24   | US-11-127-877-59<br>US-11-218-281-32   |
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| 0 1 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2  | 444                                    |

#### ALIGNMENTS

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APPLICANT: Boldog, Perence
TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoded Thereby
FILE REPERENCE: 21402-251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/10/055,877
CURRENT PELING DATE: 2002-01-22
PRIOR APPLICATION NUMBER: 0/262,892
PRIOR PELING DATE: 2001-01-19
PRIOR PILING DATE: 2001-01-3
PRIOR APPLICATION NUMBER: 60/263,598
PRIOR PILING DATE: 2001-01-23
PRIOR PILING DATE: 2001-01-24
PRIOR PILING DATE: 2001-01-24
PRIOR PILING DATE: 2001-01-24
PRIOR PILING DATE: 2001-01-25
PRIOR APPLICATION NUMBER: 60/264,117
PRIOR APPLICATION NUMBER: 60/264,117
PRIOR PILING DATE: 2001-01-25
Sequence 248, Application US/10055877
Publication No. US20050288241A1
GENERAL INFORMATION:
APPLICANT: Dedigaru, Muralidhara
APPLICANT: Padigaru, Muralidhara
APPLICANT: Miller, Charles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Vernet, Corine
Taupier Jr., Raymond
Pena, Carol
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Shimkets, Richard
Gusev, Vladimir
                                                                                                                                                                                                                                                                                                                                                                       Patturajan, Meera
Burgess, Cahterine
                                                                                                                                             Zhong, Mei
Anderson, David
Ballinger, Robert
Gerlach, Valerie
Spytek, Kimberly
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Zerhusen, Bryan
Andrew, David
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Kekuda, Ramesh
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Casman,
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112 ALLESLPPLEFSWLRTVEEGNTTVCLIDFPESSVRRSY-VLLSTLVGFVLPLLVILVCYT 170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   52 FGDALCKLVGALFVVNGYASILLLIAISIDRYLAIVHDLRYRRIRTPRRAKVLILLUWVL 111
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PRIOR PILING DATE: 2001-01-26
PRIOR PLING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: 60/263,351
PRIOR PLING DATE: 2001-03-02
PRIOR PLING DATE: 2001-03-02
PRIOR APPLICATION NUMBER: 60/275,990
PRIOR APPLICATION NUMBER: 60/275,990
PRIOR APPLICATION NUMBER: 60/275,990
PRIOR APPLICATION NUMBER: 60/275,927
PRIOR PILING DATE: 2001-03-14
PRIOR PILING DATE: 2001-03-14
PRIOR PLING DATE: 2001-03-14
PRIOR PRIOR APPLICATION NUMBER: 60/275,927
PRIOR PILING DATE: 2001-03-14
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PRIOR PILING DA
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20.7%; Score 334.5; DB 6; Length 254;
Best Local Similarity 34.1%; Pred. No. 2.2e-25;
Matches 92; Conservative 54; Mismatches 87; Indels 37;
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APPLICANT: Millar, Muralidhara
APPLICANT: Millar, Charles
APPLICANT: Tchernev, Velizar
APPLICANT: Zhong, Mei
APPLICANT: Anderson, David
APPLICANT: Ballinger, Robert
APPLICANT: Spytek, Kimberly
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Burgess, Cahterine
Eisen, Andrew
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Baumgartner, Jason
Shimkets, Richard
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ORGANISM: Artificial Sequence
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Kekuda, Ramesh
Guo, Xiaojia
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Andrew, David
Mezes, Peter
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US-10-055-877-327
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112 ALLSLPPLLFSMLRTVEEGNTTVCLIDFPEESVKRSY-VLLSTLVGFVLPLLVLLVCYT 170
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APPLICANT: Casman, Stacie
APPLICANT: Boldog, Ference
TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoded Thereby
FILE REPERENCE: 21402-251
                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: 05/2012

CURRENT PELING DATE: 2002-01-22

PRIOR PELICATION NUMBER: 60/262,892

PRIOR PELICATION NUMBER: 60/263,598

PRIOR PELICATION NUMBER: 60/263,598

PRIOR PELING DATE: 2001-01-39

PRIOR PELING DATE: 2001-01-25

PRIOR PELING DATE: 2001-01-26

PRIOR PELING DATE: 2001-01-26

PRIOR PELING DATE: 2001-01-36

PRIOR PELING DATE: 2001-01-30

PRIOR PELING DATE: 2001-01-30

PRIOR PELING DATE: 2001-03-14

PRIOR PELING DATE: 2001-03-14
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US-10-055-877-340
; Sequence 340, Application US/10055877
; Publication No. US20050288241A1
                                    Vernet, Corine
Taupier Jr., Raymond
Pena, Carol
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ORGANISM: Artificial Sequence
Gusev, Vladimir
                                                                                                                                                                                 Shenoy, Suresh
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84 SDTPLCQLSQGIYLTNRYMSISLVTALAVDRYVAVRHPLRARGLRSPRQAAAVCAVLWVL 143
                          52 PGDALCKLVGALFVVNGYASILLLTAISIDRYLAIVHPLRYRRIRTPRRAKVLILLVWVL 111
                                                                                                        144 V----IGSLVARWLLGIQEGG-----PCFRSTRHNFNSMRFPLLGFYLPLAVVVFCSL 192
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112 ALLLSIPPLIFSWIRTVEBGNITVCLIDFPEBSVKRSY-VLLSTLVGFVLPLLVILVCYT 170
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                                                                                                                                                                                                                                                    Remaining Prior Application data removed - See File Wrapper or PALM. NUMBER OF SEQ ID NOS: 127
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Leach, Martin D
APPLICANT: Shimkets, Richard A
TITLE OF INVENTION: Novel Proteins and Nucleic Acids Encoding Same
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                                                                                                                                                                                                                                                                                                                                                                  225 LLSIWRVLPTALITLWLAYVNSCLNPIIY 254
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CURRENT PEDILICATION NUMBER: US/10/877,346

CURRENT PILING DATE: 2004-06-25

PRIOR APPLICATION NUMBER: US/09/964,956

PRIOR PILING DATE: 2001-09-26

PRIOR PILING DATE: 2000-09-27

PRIOR PILING DATE: 2000-09-28

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-05

PRIOR FILING DATE: 2000-10-05
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; Sequence 83, Application US/10877346
; Publication No. US20060014153A1
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APPLICANT: Gerlach, John R
APPLICANT: Smithson, Glennda
APPLICANT: Smithson, Glennda
APPLICANT: Stone, David
APPLICANT: Stone, David
APPLICANT: Bllerman, Karen
APPLICANT: Bllerman, Karen
APPLICANT: Legley, William M
APPLICANT: Legley, Denise M
APPLICANT: Nasobrook II, John P
APPLICANT: Person Nasobrook II, John P
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Padigaru, Muralidhara
Kekuda, Ramesh
Spytek, Kimberly A
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APPLICANT: Boldog, Ference
TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoded Thereby
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20.7%; Score 334.5; DB 6; Length 254;
Best Local Similarity 34.1%; Pred. No. 2.2e-25;
Matches 92; Conservative 54; Mismatches 87; Indels 37; Gaps
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 340
LENGTH: 254
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/10/055,877
CURRENT APPLICATION NUMBER: US/10/055,877
CURRENT PILING DATE: 2002-01-22
PRIOR PILING DATE: 2001-01-9
PRIOR PILING DATE: 2001-01-9
PRIOR PILING DATE: 2001-01-24
PRIOR PILING DATE: 2001-01-24
PRIOR PILING DATE: 2001-01-24
PRIOR PILING DATE: 2001-01-25
PRIOR PILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: 60/264,478
PRIOR APPLICATION NUMBER: 60/263,351
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-03-02
PRIOR APPLICATION NUMBER: 60/275,990
PRIOR PILING DATE: 2001-03-03
PRIOR PILING DATE: 2001-03-14
PRIOR FILING DATE: 2001-03-14
PRIOR FILING DATE: 2001-03-14
PRIOR FILING DATE: 2001-03-14
  APPLICANT: DeCristofaro, Marc
APPLICANT: Pedigaru, Muralidhara
APPLICANT: Miller, Charles
APPLICANT: Tchernev, Velizar
APPLICANT: Zhong, Mei
APPLICANT: Anderson, David
APPLICANT: Ballinger, Robert
APPLICANT: Ballinger, Kamberly
APPLICANT: Ratelli, Luca
APPLICANT: Ratelli, Luca
APPLICANT: Retelli, Luca
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Gusev, Vladimir
Vernet, Corine
Taupier Jr., Raymond
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Burgess, Cahterine
Bisen, Andrew
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Baumgartner, Jason
                                                                                                                                                                                                                                                                                                                    Guo, Xiaojia
Zerhusen, Bryan
Andrew, David
Mezes, Peter
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Adam
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APPLICANT:
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US-11-127-877-52

Sequence 52, Application US/11127877

Sequence 52, Application Woll1127877

Sequence 52, Application Woll1127877

Sequence 52, Application Woll2287565A1

GREERAL INFORMATION:
APPLICANT: Merchiers, Pascal G.
APPLICANT: Laenen, Wendy

TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting

TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting

FILE REFERENCE: P27, 800-B USA

CURRENT APPLICATION NUMBER: US/11/127,877

CURRENT PILING DATE: 2006-05-12

FRIOR FILING DATE: 2006-05-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        194 VVTALAQRPPTDVGQAEATRKAARMVWANILVFVVCFLPLHVGLTV----RLAVGWNACA 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  :| : :| || || || || || || 280 VLNIVNVVYKVTRPLASANSCLDPVLYLLITGDKYRRQLRQLCGGGKPQPRTAASSLALVS 339
44 VVFVLGLGLNAPTLMLFIFRLRPWDATATYMFHLALSDTLYVLSLPTLIYYAAHNHWPF 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 88 ---LCQLSQGIYLTNRYMSISLVTAIAVDRYVAVRHPLRARGLRSPRQAAAVCAVLWVLV 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     145 IGSLVAR-WLLGIQEGG---FCFRSTR----H--NFNSMRFPLLGFYLPLAVVVFCSLK 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              250 LLETIRRALYITSKLSDANCCLDAICYYYMAKERQE-------ASALAVAP 293
                                                                                                                                                                                                                 Sequence 545, Application US/10995561
Publication No. US20050272054A1
GENERAL INFORMATION:
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REPERENCE: CLOO1559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT PILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29 VILVIGILINSLALMVFCCRMQQWTETRIYMTNLAVADLCLLCTLPFVLHSLRDTSDTP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    45; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 365;
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19.5%; Score 315.5; DB 6;
Best Local Similarity 29.1%; Pred. No. 2.3e-23;
Matches 93; Conservative 55; Mismatches 127;
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                                                               286 -ASALAVAPRAKA 297
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US-10-995-561-545
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LENGTH: 365
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        115 YVAVRHPLRARGLRSPRQAAAVCAVLWVLVIGSLVARWLLGIQEGG---FCFRSTRHNFN 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMRFP----LLGFYLPLAVVVFCSLKVVTALAQRPPTDVGQAEATRKAARMVWANLLVF 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     227 VVCPLPLHVGLTVRLAVGWNACALLETIRRALYITSKLSDANCCLDAICYYYMAKEPQE- 285
                                                                                                                                                                                                                                               52 FGDALCKLVGALFVVNGYASILLLITAISIDRYLAIVHPLRYRRIRTPRRAKVLILLUWVL 111
                                                                                                                                                                                                                                                                                                              144 V----IGSLVARWLLGIQEGG-----FCFRSTRHNFNSMRFPLLGFYLPLAVVVFCSL 192
                                                                                                                                                                                                                                                                                                                                                                                                   193 KVVTALAQRPPTDVG---QABATRKAARMVWANLLVFVVCFLPLHVGLTVRLAVGWNACA 249
                                                                                                                                                                                                                                                                                                                                                                                                                            60 TNLAVADLCLLCTLPF-VLHSLRDTS----DTPLCQLSQGIYLTNRYMSISLVTAIAVDR 114
                                                                                                                                                                                                                     84 SDTPLCQLSQGIYLTNRYMSISLVTAIAVDRYVAVRHPLRARGLRSPRQAAAVCAVLWVL 143
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                                                                                                                                                                             21
                                                                                                                                                             28 GVLLVLGLLLNSLALWVPCCRMQQWTBTRIYMTNLAVADLCLLCTL-PFVLHSLRD---T
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                                                                                        Gaps
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                                                                                      37;
                                        20.7%; Score 334.5; DB 6; Length 254; 34.1%; Pred. No. 2.2e-25; ive 54; Mismatches 87; Indels 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 346;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Regulation of Human CysLT2-Like GPCR;
TITLE OF INVENTION: Protein
TITLE OF INVENTION: Protein
FILE REPERENCE: 04974.00458
CURRENT FILING DATE: 2005-06-22
CURRENT FILING DATE: 2005-06-22
PRIOR APPLICATION NUMBER: US/09/828,478
PRIOR FILING DATE: 2001-04-09
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FaelSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LLETIR---RALYITSKLSDANCCLDAICY 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 2, Application US/11157930; Publication No. US20050266482A1; GENERAL INFORMATION:
                                                               34.1%;
                                                                                        92; Conservative
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                                                               Best Local Similarity
    JS-10-877-346-83
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                                                                                                                                                                                                                                                                                                                                                                                                                       150 LVSIDRYLALVKTMSMGRARGVRWAKLYSLVIWGCTLLLSSPMLVFRTMKEYSDEG---- 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRHN------FNSMRFPLLGFYLPLAVVVFCSLKVVTALAQRPPTDVGQA 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         206 ---HNVTACVISYPSLIWEVFTNMLLNVVGFLLPLSVITFCTMQIMQVLRNNEMQXFKBI 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EATRKAARMYWANLLVFVVCFLPLHVGLTV----RLAVGWNACALLETIRRALYITSKLS 265
                                                                                                                                                                                                                                                                                                                          53 TETRIYMTNIAVADLCLLCTLPFVLHSLRDTSD----TPLCQLSQGIYLTNRYMSISLVT 108
                                                                                                                                                                                                                                                                                                                                                                                               109 AIAVDRYVAVRHPLRARGLRSPRQAAAVCAVLW--VLVIGS--LVARWLLGIQEGGFCFR 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   263 QTERRATVLVLVVLLFIICWLPPQISTFLDTLHRLGI-LSSCQDERIIDVITQIASFMA 321
                                                                                                                                                                                                                                                                                       38 INGTPAQSKCPQVEWLGWINTIQPP-----PLWVLPVLATLENIFVLSVFCLHKSSC 89
                                                                                                                                                                                                                                                        1 MNGTYNTCGSSDLTW-----PPAIKLGFYAYLGVLLVLGLLLNSLALWVFCCRMQQW 52
                                                                                                                                                                                                                    51;
                                                                                                                                                                                     Length 391;
                                                                                                                                                                                 19.4%; Score 312.5; DB 7; Length 3 27.6%; Pred. No. 4.9e-23; tive 54; Mismatches 128; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    266 DANCCLDAICYYYMAKEPOEAS 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        322 YSNSCLNPLVYVIVGKRFRKKS 343
PRIOR APPLICATION NUMBER: 60/603,948
PRIOR FILING DATE: 2004-08-24
NUMBER OF SEQ ID NOS: 590
SOFTWARE: Patentin version 3.3
SEQ ID NO 52
LENGTH: 391
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APPLICANT: Decristofaro, Marc
APPLICANT: Padigaru, Muralidhara
APPLICANT: "Aller, Charles
APPLICANT: "Aller, Charles
APPLICANT: Anderson, David
APPLICANT: Anderson, David
APPLICANT: Ballinger, Robert
APPLICANT: Sprek, Kimberly
APPLICANT: Retelli, Luca
APPLICANT: Retelli, Luca
APPLICANT: Retelli, Luca
APPLICANT: Retelli, Luca
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Vernet, Corine
Taupier Jr., Raymond
Pena, Carol
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Patturajan, Mera
Burgess, Cahterine
Eisen, Andrew
Wolenc, Adam
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Shimkets, Richard
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Zerhusen, Bryan
Andrew, David
                                                                                                                                                                                                                        Conservative
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                                                                                                               TYPE: PRT
ORGANISM: Homo sapiens
US-11-127-877-52
                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 89; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Casman, S
Boldog,
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US-10-055-877-225
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APPLICANT:
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86 ----TPLCQLSQSIYLTNRYMSISLVTAIAVDRYVAVRHPLRARGLR-SPRQAAAVCAVL 140
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                                                          CURRENT APPLICATION NUMBER: 05/20,877

CURRENT FILING DATE: 2002-01-22

PRIOR PELICATION NUMBER: 60/262,892

PRIOR PILING DATE: 2001-01-19

PRIOR PILING DATE: 2001-01-19

PRIOR PILING DATE: 2001-01-23

PRIOR PILING DATE: 2001-01-24

PRIOR PILING DATE: 2001-01-24

PRIOR PILING DATE: 2001-01-24

PRIOR PILING DATE: 2001-01-24

PRIOR PILING DATE: 2001-01-25

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PRIOR PLING DATE: 2001-01-25

PRIOR PLING DATE: 2001-01-26

PRIOR PLING DATE: 2001-01-26

PRIOR PLING DATE: 2001-01-36

PRIOR PLING DATE: 2001-01-30

PRIOR PLING DATE: 2001-03-02

PRIOR PLING DATE: 2001-03-02

PRIOR PLING DATE: 2001-03-14

PRIOR PLING DATE: 2001-03-14
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Best Local Similarity 33.0%; Pred. No. 1.6e-22;
Matches 93; Conservative 49; Mismatches 84; Indels
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APPLICANT: Padigaru, Muralidhara
APPLICANT: Miller, Charles
APPLICANT: Tchernev, Velizar
APPLICANT: Zhong, Mei
APPLICANT: Ballinger, Robert
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179 GFYLPLAVVVFCSLKVVTALAQRPPTDVGQAEATRKAARMVWANLLVFVVCFLPLHVGL- 237
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Best Local Similarity 29.1*
Matches 88; Conservative
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ORGANISM: Homo sapiens
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TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoded Thereby
FILE REFERENCE: 2.04.02.251

CURRENT APPLICATION NUMBER: 06/262,892

PRIOR PILING DATE: 2001-01.9

PRIOR PILING DATE: 2001-01.9

PRIOR PILING DATE: 2001-01.23

PRIOR PILING DATE: 2001-01.24

PRIOR PILING DATE: 2001-01.25

PRIOR PILING DATE: 2001-01.25

PRIOR PILING DATE: 2001-01.25

PRIOR PILING DATE: 2001-01.25

PRIOR PILING DATE: 2001-01.26

PRIOR PILING DATE: 2001-01.30

PRIOR PILING DATE: 2001-01.30

PRIOR PILING DATE: 2001-03-02

PRIOR PILING DATE: 2001-03-04

PRIOR PILING DATE: 2001-03-04

PRIOR PILING DATE: 2001-03-14

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18.9%; Score 305; DB 6; Length 259;
Best Local Similarity 33.0%; Pred. No. 1.6e-22;
Matches 93; Conservative 49; Mismatches 84; Indels 56; Gaps
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NUMBER OF SEQ ID NOS: 512
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                 Vernet, Corine
Taupier Jr., Raymond
Pena, Carol
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Burgess, Cahterine
Eisen, Andrew
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Shimkets, Richard
Gusev, Vladimir
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Gerlach, Valerie
Spytek, Kimberly
Ratelli, Luca
Kekuda, Ramesh
                                                                          Guo, Xiaojia
Zerhusen, Bryan
Andrew, David
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                                                                                                                                                                                                                           Wolenc, Adam
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Casman,
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LENGTH: 259
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120 HPLRARGLRSPROAAAVCAVLWVLVIGS----LVARWLLGIQEGGFCF----RSTRHNF 170
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                                                                                   238 --TVRLAVGWNA-CALLETIRRALYITSKLSDANCCLDAICY 276
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SEQ ID NO 66
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APPLICANT: Hoffmann, Marcel
APPLICANT: Spittaels, Koenraad F. F.
APPLICANT: Spittaels, Koenraad F. F.
APPLICANT: Laenen, Wendy
TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
TITLE OF INVENTION: Amyloid-Beta Protein Production
FILE REPERENCE: P27, 800-8 USA
CURRENT PILING DATE: 2005-05-12
FRIOR PILING DATE: 2004-05-12
PRIOR FILING DATE: 2004-05-12
PRIOR FILING DATE: 2004-08-24
NUMBER OF SEQ ID NOS: 590
SOFTWARE Patentin Version 3.3
SEQ ID NO 46
LENGTH: 373
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                                                                                                                                                                                                                                                                                                                                                                                                                                       103 VADLSCVLVLPTRLVYHFSGNHWPFGBIACRLTGFLFYLNMYASIYFLTCISADRFLAIV 162
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CURRENT APPLICATION NUMBER: US/11/157,930
CURRENT FILING DATE: 2005-06-22
PRIOR APPLICATION NUMBER: US/09/828,478
PRIOR PILING DATE: 2001-04-09
PRIOR PLING DATE: 2000-04-07
PRIOR PLING DATE: 2000-04-07
PRIOR PLING DATE: 2000-12-13
NUMBER: OS SEQ ID NOS: 16
SEQ ID NO 6
SEQ ID NO 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EA 286
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                                                                                                                                                                                                                                               US-11-157-930-6
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18.5%; 26.2%;

Query Match Best Local Similarity

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y CARLEANT: Marchials, Rescal G.
APPLICANT: Hoffmann, Marcel
APPLICANT: Hoffmann, Marcel
APPLICANT: Spittaels, Koenraad F. F.
APPLICANT: Spittaels, Koenraad F. F.
APPLICANT: Laenen, Wendy
TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
FILE REFERENCE: P27, 800-B USA
CURRENT APPLICATION NUMBER: US/11/127,877
CURRENT FILING DATE: 2005-05-12
PRIOR PILING DATE: 2004-06-12
PRIOR PILING DATE: 2004-06-12
PRIOR FILING DATE: 2004-06-24
NUMBER OF SEQ ID NOS: 590
SOFTWARE: Patentin version 3.3
                                                                                                                                                                                                                                                                                                                                                                               213
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94 NLVVTDLLVGLSLPTRFAVYYGARGČLRČAFPHVLG---------YFLNMHC 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     103 SISLVTAIAVDRYVAVRHPLRARGLRSPRQAAAVCAVLWVLVIGSLVARWLLGIQEGGFC 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  105 SLVTAIAVDRYVAVRHPLRARGLRSPRQAAAVCAVLWVLV---IGSLVARWLLGIQEGG- 160
                                                                                                                                                                                                                                                                                                   200 ITCYDITSDEYLRSYFIXSMCITVAMFCVPLVLILGGYGLIVRALIXK---DLDNSPLRR 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SILPLICICVDRYLAIVRPEAPAACROPACARAVCAFVW-LAAGA-VILSVLGVIGSRPC 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                163 FRSTRHNFNSMRFPLLGFYLPLAVVVFCSLKVVTALAQRPPTDVGQAEATR-KAARMVWA 221
                                                                                                                                                                                       49 MQQWTETRIYMTNLAVADLCLLCTLPFVLHSLRDTSD----TPLCQLSQGIYLTNRYMSI 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MNGTYNTCGSSDLTWPPAIKLGFYAYLGVLLVLGLLLNSLALWVFCCRMQQWTFTRIYMT 60
                                                                               20 GPGSSWGNSTVASTAAVSSSFKCALTKTGFQFYYLPAVYILVFIIGFLGNSVAIWMFVFH 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   214 KAARMVWANILLVFVVCFLPLHVGLTVRLAVGWN-----ACALLETIRRALYITSKLSDAN
                                                                                                                                                                                                                                                                                                                                                                               161 -PCFRSTRHNF----NSMRFPLLGFYLPLAVVVFCSLKVVTALAQRPPTDVGQAEATR
                                                  GTYNTCGSSDLTWPPAI-----KLGF-YAYLG----VLLVLGLLLNSLALWVFCCR
39; Gaps
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Indels
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18.4%; Score 297.5; DB 7;
Best Local Similarity 29.4%; Pred. No. 1.3e-21;
Matches 89; Conservative 42; Mismatches 111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      269 CCLDAICYYYMAKEFQEASALAVAPRAKAHKSQDSL 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         317 SCVDPILYFLAGDTFRR--RLSRATRKASRRSEANL 350
  Mismatches 137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 66, Application US/11127877; Publication No. US20050287565A1; GENERAL INFORMATION:
  72;
     88; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-127-877-66
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completed: February
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Job time : 11.5 secs
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TITLE OF INVENTION: GRNETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REFERENCE: CL001559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT PILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FactSEQ for Windows Version 4.0
SEQ ID NO 523
LENGTH: 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             205 LPLLVMVICYSGILKTLIR----CRNEKKRHRAVRLIFTIMIVYFLFWAPYNIVLLINT 259
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    133 AAAVCAVLWVL-VIGSLVARWLLGIQEGGFCFRSTRH------NFNSMRFPLLGFY 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LPLAVVVFCSLKVVTALAQRPPTDVGQAEATRKAARMVWANLLVFVVCFLPLHVGL---T 238
NLLVFVVCFLPLHVGLTVRLAVGWNACALLETIRRALYITSKLSDANCCLDAICYYYMAK 281
                          246 VLIIFLVCPTPFHAR---QVAVALWPDMPHHTSLVVYHVAVTLSSLNSCMDPIVYCFVTS 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34 PPLYSLVPIPGFVGNMLVILILIN-----CKRLKSMTD--IYLLNLAISDLFFLLTVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16 PPAINTGF-YAYLGVLLVLGLLLNSLALWVFCCRMOOWTETRIYMTNLAVADLCLLCTLP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/11068686
Publication No. US20050260565A1
GENERAL INFORMATION:
APPLICANT: Gray, Patrick W.
Schweickart, Vicky L.
TITLE OF INVERTY, Carol J.
TITLE OF INVERTY: Chemokine Receptor Materials and Methods
NUMBER OF SEQUENCES: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSER: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 S. Wacker Drive
CITY: Chicago
STATE: 11linois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match , 17.9%; Score 288.5; DB 6; Length 352; Best Local Similarity 26.2%; Pred. No. 9.2e-21; Matches 75; Conservative 62; Mismatches 118; Indels 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               260 FQEFFGLNNCSSSNRLDQAMQVIETLGMTHCCINPIIYAFVGEKFR 305
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                                                                                                                                                                                                                               ; Sequence 523, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
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COMPUTER READABLE FORM:
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CRGANISM: Homo sapiens
US-10-995-561-523
                                                                                    282 EFQ 284
                                                                                                                           303 GPQ 305
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US-11-068-686-2
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9, 2006, 01:21:41

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75 FVLHSLRDTSD--TPLCQLSQGIYLTNRYMSISLVTAIAVDRYVAVRHPLRARGLRSPRQ 132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               145 GVVTSVITWVVAVPASLPGIIFTRRQKRGLHYTCSSHPPYSQYQFWKNPQTLKIVILGLV 204
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          84
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        239 VRLAVGWNACALLETIRRALYITSKLSDANCCLDAICYYYMAKEFQ 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
17.9%; Score 288.5; DB 7; Length:
Best Local Similarity 26.2%; Pred. No. 9.2e-21;
Matches 75; Conservative 62; Mismatches 118; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc feature
OTHER INFORMATION: /= "88C amino acid sequence"
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: PatentIn Release #1.0, Version #1.30
                                                            LENGTH: 352 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-11-068-686-2
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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- protein search, using sw model OM protein

Pebruary 9, 2006, 00:47:43 ; Search time 165 Seconds
(without alignments)
1321.262 Million cell updates/sec Run on:

US-10-083-168-16 1614 1 MNGTYNTCGSSDLTWPPAIK......AVAPRAKAHKSQDSLCVTLA 309 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2166443 segs, 705528306 residues Searched:

2166443 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt\_05.80:\*
1: uniprot\_sprot:\*
2: uniprot\_trembl:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

|           |        | Description     | у            | homo        | homod        | homo         | homo         | mus r       | Q5ku21 homo sapien | _            | _            |              | homo         | рошо        | рошо         | _            | _            |              | homo        |              | gallı       | homo        | _            |              |            |              | homo        | рошо         |             | mus 1       | Q4g072 rattus norv | Q53fa0 homo sapien | Q9ep66 mus musculu |  |
|-----------|--------|-----------------|--------------|-------------|--------------|--------------|--------------|-------------|--------------------|--------------|--------------|--------------|--------------|-------------|--------------|--------------|--------------|--------------|-------------|--------------|-------------|-------------|--------------|--------------|------------|--------------|-------------|--------------|-------------|-------------|--------------------|--------------------|--------------------|--|
| SUMMARIES |        | ΙD              | Q6FHI8 HUMAN | GPR35 HUMAN | Q42FV2 HUMAN | Q6ZMP9 HUMAN | Q4VBN5_HUMAN | GPR35 MOUSE | QSKU21_HUMAN       | Q8CB97 MOUSE | Q8BS98_MOUSE | Q4TAHO_TETNG | Q502U9_HUMAN | P2RY9 HUMAN | Q6NSP5_HUMAN | Q8BKK1 MOUSE | Q8BLG2 MOUSE | Q4S8W3_TETNG | GPRSS HUMAN | Q8TDS4 HUMAN | P2RY5 CHICK | G109B_HUMAN | Q8NGE4 HUMAN | Q7ZZA4_BRARE | Q9WU09_RAT | Q4RPP7_TETNG | GPR92 HUMAN | Q5KU18 HUMAN | P2RYS HUMAN | P2RY5 MOUSE | Q4G072 RAT         | Q53FA0 HUMAN       | Q9EP66_MOUSE       |  |
|           |        | 03              | 8            | Н           | 7            | 7            | 7            | Н           | ~                  | ~            | ~            | ~            | 0            | Н           | 7            | 7            | 7            | ~            | ٦           | ~            | Н           | -           | ~            | ~            | ~          | N            | Н           | 7            | Н           | -           | ~                  | 7                  | 7                  |  |
|           |        | Match Length DB | 309          | 309         | 309          | 394          | 308          | 307         | 307                | 307          | 307          | 305          | 370          | 370         | 370          | 370          | 370          | 302          | 319         | 363          | 308         | 387         | 387          | 347          | 296        | 345          | 372         | 372          | 344         | 344         | 344                | 344                | 360                |  |
| •         | ouery  | Match           | 99.6         | 99.3        | 99.3         | 99.3         | 98.9         | 9.69        | 9.69               | 9.69         | 68.7         | 25.9         | 25.0         | 24.9        | 24.8         | 24.8         | 24.3         | 23.3         | 23.3        | 23.3         | 22.8        | 22.8        | 22.8         | 22.8         | 22.6       | 22.6         | 22.4        | 22.4         | 22.4        | 22.1        | 22.1               | 22.0               | 21.6               |  |
|           |        | Score           | 1608         | 1602        | 1602         | 1602         | 1597         | 1124        |                    |              | 1109         | 4            |              |             | 400          | 400          | 392          | 376.5        | 376         | 375.5        | 368.5       | 368.5       | 368.5        | 368          | 365.5      | 365          | 362         | 362          | 361.5       | 357.5       | 356                | 355.5              | 348.5              |  |
|           | Result | No.             |              | 7           | m            | 4            | v            | 9           | <u></u>            | 8            | 60           | 10           | -            | 12          | 13           | 14           | 15           | 16           | 17          | 18           | 19          | 20          | 21           | 22           | 23         | 24           | 25          | 56           | 27          | 28          | 29                 | 30                 | 31                 |  |

| 50 2 Q4SPQ4 TETNG 50 2 Q80Z39_RAT 61 P P2RY2 RAT 71 P2RY2 RAT 71 1 P2RY2 HUNAN 15 Q4VBN1 HUNAN 15 Q4VBN1 HUNAN 15 Q5XG6_XENLA 16 1 GPR81 HUNAN 15 1 CLTR2_PIG 16 GPR81 MOUSE 13 1 P2RY4 RAT 15 Q5YA25_PIG 17 Q5YA25_PIG 18 1 P2RY4 RAT 18 1 Q5YA25_PIG 19 Q5YA25_PIG 10 G5YA25_PIG 10 G5YA25_PIG 11 P2RY4 RAT 12 Q5YA25_PIG 13 Q5YA25_RAT  | Q4spq4 tetracdon n<br>Q80239 rattus norv<br>P41232 rattus norv<br>Q8ve54 mus musculu<br>P41231 homo sapien<br>Q4vbnl homo sapien<br>Q5xg6 xenopus lae<br>Q9bxc0 homo sapien<br>Q9bxc0 homo sapien<br>Q9c3311 rattus norv<br>Q5ya25 sus scrofa |
|--|---|
| 288 25 25 25 25 25 25 25 25 25 25 25 25 25   | 048PQ4 TETNG 080239_RAT 080723 PRAT 0807254_MOUSE P2RY2 HUMAN 04VBN1_HUMAN 05XCS6_XENLA 05XCS6_XENLA 05RS1 HUMAN 0LTR2_PIG 06PS81_MOUSE 05R81_MOUSE 05R81_MOUSE 05RX4_RAT 05YA25_PIG 05YA25_PIG   |
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Warren C.N., Aronstam R.S., Sharma S.V.;

"cDNA clones of human proteins involved in signal transduction

"cDNA clones of human proteins involved in signal transduction

"equenced by the Guthrie cDNA resource center (www.cdna.org).";

Submitted (ARR-2003) to the EMBL/GenBank/DDBJ databasses.

-!- FUNCTION: Orphan receptor.

-!- FUNCTION: Orphan receptor.

-!- SUBCELLUIAR LOCATION: Integral membrane protein (By similarity).

-!- SIBSUE SPECIFICITY: Expressed in all adult and fetal tissues

examined, including pancreatic islets and skeletal muscle, with

relatively higher levels in adult lung, small intestine, colon and
                                                                                                                                                                                                                                                                           Bukaryoča, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUCLEOTIDE SEQUENCE, AND VARIANTS THR-25; ILE-29; MET-108; SER-125 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Genetic variation in the gene encoding calpain-10 is associated with type 2 diabetes mellitus.";
Nat. Genet. 26:163-175(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=20472315; PubMed=11017071; DOI=10.1038/79876; Horikawa Y., Oda N., Cox N.J., Li X., Orho-Melander M., Hara M., Hinoko Y., Lindner T.H., Mashima H., Schwarz P.B.H., Gel Bosque-Plata L., Horikawa Y., Oda Y., Yoshiuchi I., Colilla Spolonsky K.S., Wei S., Concannon P., Iwasaki N., Schulze J., Baier L.J., Bogardus C., Groop L., Boerwinkle E., Hanis C.L.,
                                                                                                                                                                                                                                                                                                                                               WUCLEOTIDE SEQUENCE, AND VARIANT ARG-294.
MEDLINE=98140132; PubMed=9479505; DOI=10.1006/geno.1998.5095; O'Dowd B.F., Nguyen T., Marchese A., Cheng R., Lynch K.R., Heng H.H.Q., Kolakowski L.F. Jr., George S.R.; "Discovery of three novel G-protein-coupled receptor genes."; Genomics 47:310-313(1998).
                                                                                                                                                       GPR35 HUMAN STANDARD; PRT; 309 AA. 09HC97; 043495; Q86UH4; 16-OCT-2001 (Rel. 40, Created) 11-SEP-2005 (Rel. 48, Last sequence update) 11-SEP-2005 (Rel. 48, Last annotation update) Probable G-protein coupled receptor 35.
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EMBL; AF089087; AAG17965.1; -; mENA.
EMBL; AY275467; AAP32299.1; -; Genomic_DNA.
Ensembl; ENSG00000178623; Homo sapiens.
HGNC; HGNC:4492; GPR35.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 PLRARGLRSPROAAVCAVLWULVIGSLVARWILGIQEGGFCFRSTRHNFNSMRFPLLGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 PLRARGLRSPRQAAAVCAVLWVLVIGSLVARWLLGIQBGGFCPRSTRHNFNSMAFPLLGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
Pfam, PF00001; 7tm 1; 1.

PROMING, PRO0237; GPCRRHODOPSN.

PROSITE; PS00237; GPCREIN RECEP_F1_1; 1.

PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.

PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.

Transducin coupled receptor; Glycoprotein; Polymorphism; Receptor; Transducer; Transmembrane.

Extracellular (Potential).
                                                                                                                                                                                                                                                                                                                                                                       // (Potential).
Cytoplasmic (Potential).
N-linked (GlcNAc. . .) (Potential).
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0; Mismatches 2: 7-3-7
                                                                                                                                                                                                                                                                   Extracellular (Potential).
                                                                                                                                                                                                                                                                                     5 (Potential).
Cytoplasmic (Potential).
6 (Potential).
Extracellular (Potential).
                                                                                                                                 1 (Potential).
Cytoplasmic (Potential).
2 (Potential).
Extracellular (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /FTId=VAR_013606.
4 -> R (in Ref. 1).
97734FB7231B26F0 CRC64;
                                                                                                                                                                                                                            Cytoplasmic (Potential).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FTIG=VAR_013603.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FTIG=VAR_013604.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              r -> M.
/FTId=VAR_013605.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        FTIG=VAR_013601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FTIG=VAR_013602.
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                                                                                                                                                                                                              (Potential).
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                                                                                                                                                                                                                                                                                                                                                                  (Potential)
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34072 MW;
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Matches 307; Conservative
                                                                                                                                                                                                                                                                                                                            233
258
309
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Nouzelania September.

Rawakami B., Sugiyama A., Takemoto M., Sugiyama T., Irie R.,

Rawakami B., Sugiyama A., Takemoto M., Sugiyama T., Irie R.,

Rawakami B., Sugiyama A., Takemoto M., Sugiyama T., Irie R.,

Rawakami T., Sato H., Ota T., Wakamatsu A., Ishii S., Yamamoto J.,

Rawati T., Sato H., Ota T., Wakamatsu T., Kimura K.,

Isono Y., Kawai-Hio Y., Saito K., Nishikawa T., Kimura K.,

Namashita H., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K.,

Ramashita H., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K.,

Ramashita H., Matsuo K., Nakamura Y., Sakine M., Kikuchi H., Kanda K.,

Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.

I- SIMILARITY: Belongs to the G-protein coupled receptor I family.

Shambi EMSCO000017862; Homo sapiens.

CO: GO:00016021; C:integral to membrane; IEA.

GO: GO:000184; F:receptor activity; IEA.

GO: GO:000184; F:rhodopsin-like receptor protein signalin. .; IEA.

GO: GO:000184; F:rhodopsin-like receptor protein signalin. .; IEA.

CO: GO:000184; F:rhodopsin-like receptor protein signalin. .; IEA.

RANTE, PRO0237; GPRCRHIN RECEP FI 1; 1.

RRINTS; PRO0237; GPRCRHIN RECEP FI 1; 1.

RRINTS; PRO0237; GPRCRHIN RECEP FI 1; 1.

RRINTS; PRO0237; GPRCRHIN RECEP FI 2; 1.

RRINTS; PRO0237; GPRCRHIN RECEP FI 2; 1.

G-protein coupled receptor; Transducer; Transmembrane.

SEQUENCE 394 AA; 43309 MW; 1558FD44BAE4233C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YLPLAVVVFCSLKVVTALAQRPPTDVGQAEATRKAARMVWANLLVFVVCFLPLHVGLTVR 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 NLAVADICILICTEPFVIHSERDTSDTPLCQLSQGIYLTNRYMSISLVTAIAVDRYVAVRH 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LAVGWNACALLETIRRALYITSKLSDANCCLDAICYYYMAKEFQEASALAVAPRAKAHKS 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PLRARGLRSPRQAAAVCAVLWVLVIGSLVARWLLGIQEGGFCFRSTRHNFNSMRFPLLGF
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                                  Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MNGTYNTCGSSDLTWPPAIKLGFYAYLGVLLVLGLLLNSLALWVFCCRMQQWTETRIYMT
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99.3%; Score 1602; DB 2; Length 3
99.4%; Pred. No. 6e-112;
ive 0; Mismatches 2; Indels
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Last annotation update)
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Hypothetical protein FLJ16773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-SEP-2005 (TrEMBLrel. 31, 13-SEP-2005 (TrEMBLrel. 31, 13-SEP-2005 (TrEMBLrel. 31, 13-SEP-2005 (TrEMBLrel. 31,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GPR35 protein (Fragment).
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Q4VBNS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 99.4 Matches 307; Conservative
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                                                                                                                                                      NUCLEOTIDE SEQUENCE.
                         Homo sapiens (Human)
                                                                                                       NCBI_TaxID=9606;
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                                                                                     Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wilson R.K.;
Submitted (ARR-2005) to the EMBL/GenBank/DDBJ databases.
Submitted (ARR-2005) to the EMBL/GenBank/DDBJ databases.

-1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
-1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.

EMBL; AC124662; AAX88945.1; -; Genomic_DNA.
InterPro, 1PR000276; GPCR_Rhodpsn.
PRAM: PR00001; 7tm 1; 1.

PRINTS; PR00237; GPCRRHODOPSN.
PROSITE; PS00237; GPCRRHODOPSN.
PROSITE; PS00237; GPCTEIN RECEP_F1 1; 1.

G-protein coupled receptor; Hypothetical protein; Receptor;
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99.3%; Score 1602; DB 2; Length 309;
Best Local Similarity 99.4%; Pred. No. 4.9e-112;
Matches 307; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                         Haakenson W., Trani L., Schatzkamer K.;
"The sequence of Homo sapiens BAC clone RP11-27M15.";
Submitted (JUN-2002) to the BMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                            to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                  to the EMBL/GenBank/DDBJ databases
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Last annotation update)
      Last annotation update)
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Q6ZMP9;
      13-SEP-2005 (TrEMBLrel. 31 Hypothetical protein GPR35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Transducer; Transmembrane.
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                                                                                                                                                                                                                                                                                                                                            Waterston R.H.;
Submitted (SEP-2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                    Waterston R.;
Submitted (OCT-2002)
                                                                       Homo sapiens (Human)
                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                                             NUCLEOTIDE SEQUENCE.
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                                                                                                                                                             NCBI_TaxID=9606;
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05-JUL-2004 (
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Gaps

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205 180 265

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385

RESULT Q6ZMP9 1 ID Q6 AC Q6 DT 05 DT

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                                           TISSUE-G-protein coupled receptors;

WEDLINE=22388257, PubMed=12477932; DOI=10.1073/pnas.242603899;

WEDLINE=22388257, PubMed=12477932; DOI=10.1073/pnas.242603899;

WETAUSDERG R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Mopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,

A stapleton M., Scares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

B rownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,

R Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

B Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

R Pahey J., Helton E., Ketreman M., Madan A., Rodrigues S., Sanchez A.,

M Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

B Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

R Rohlerchield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

B Chair D. Schain J.E., Jones S.J.M., Marra M.A.,

R Generation and initial analysis of more than 15,000 full-length human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LPLAVVVPCSLKVVTALAQRPPTDVGQAEATRKAARWWANLLVPVVCFLPLHVGLTVRL 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         241 AVGWNACALLETIRRALYITSKLSDANCCLDAICYYYMAKEPQEASALAVAPSAKAHKSQ 300
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Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NGTYNTCGSSDLTWPPAIKLGFYAYLGVLLVLGLLLNSLALWVFCCRMQQWTETRIYMTN
                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
--- SUBCELLUAR LOCATION: Integral membrane protein (By similarity).
--- SUMILBRITY: Belongs to the G-protein coupled receptor 1 family.
EMBL; BC095500; AAH955001; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Pfam; PF00001; 7tm 1; 1.
PRINTS; PR00237; GPCRHODOPSN.
PROSTIE; PS00237; GPROTEIN RECEP_F1_1; 1.
PROSTIE; PS50262; G_PROTEIN RECEP_F1_2; 1.
G-protein coupled receptor; Receptor; Transducer; Transmembrane.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98.9%; Score 1597; DB 2; Length 308; 99.4%; Pred. No. 1.1e-111;
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                                                                                                                                                                                                                                                                                                                                          and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
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NIH MGC Project;
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                          TaxID=9606,
                                                     NUCLEOTIDE
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STRAIN-ESTBL/63; TISSUE-AMERICAN GLAND, STRAIN-ESTBL/63; TISSUE-AMERICAN GLAND, STRAIN-ESTBL/63; TISSUE-AMERICAN GLAND, STRAIN-ESTBL/63; PubMede12479932; DOI=10.1073/pnas.242603899; Strausberg R.L., Felingold E.A., Grouse L.H., Derge J.G., Schuler G.D., Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Diatchenko L., Marueina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Carsinori P., Prange C., Arpleton M., Soares M.B., Bonaldo M.F., Carninori P., Prange C., Arpleton M.J., Perers G.J., Abramson R.D., Mullahy S.J., Bonak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunarathe P.H., N. McZhang S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M., Pilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Malterfield Y.S.N., Krzywinski M.I., Skalaka U., Smailus D.E., Butterfield Y.S.N., Krzywinski M.I., Skalaka U., Smailus D.E., Schnerch A., Schein J.B., Jones S.J.M., Marra M.A.;
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                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Genetic variation in the gene encoding calpain-10 is associated with
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

-!- FUNCTION. Orphan receptor.

-!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).

-!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUCLECTIDE SEQUENCE.
MEDLINE=20472315; PubMed=11017071; DOI=10.1038/79876;
MEDLINE=20472315; PubMed=11017071; DOI=10.1038/79876;
Hinorikawa Y., Cda N., Cox N.J., Li X., Orho-Melander M., Hara M.,
Hinorikawa Y., Lindner T.H., Mashima H., Schwarz P.E.H.,
del Bosque-Plata L., Horikawa Y., Oda Y., Yoshiuchi I., Colilla Polonsky K.S., Wei S., Concannon P., Iwasaki N., Schulze J.,
Paler L.J., Bogardus C., Groop L., Boerwinkle E., Hanis C.L.,
                                                                          16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
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EMBL; BC027429; AAH27429.1; -; mRNA.
Ensembl; ENSWUSG0000026271; Mus musculus.
MGI; MGI:1929509; Gpr35.
GO; GO:0016021; C:integral to membrane; TAS.
InterPro; IPR00276; GPCR_Rhodpsn.
307 AA.
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                                                                                                                                                                                                                     Probable G-protein coupled receptor 35.
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PRINTS, PR00237, GPCRRHODOPSN.
PRINTS, PR01157, P2YPURNOCPTR.
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    STANDARD;
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                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10090;
    GPR35_MOUSE
                                                                                                                                                                                                                                                                         Name=Gpr35;
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QECB97 MOUSE PRELIMINARY;
Q8CB97;
                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GFYLPLAVVVFCSLKVVTALAQRPPTDVGQAEATRKAARMVWANLLVFVVCFLPLHVGLT 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VRLAVGWNACALLETIRRALYITSKLSDANCCLDAICYYYMAKEFQEASALAVAPRAKAH 298
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Bukaryota, Metazoa, Chordata, Craniata, Primates, Catarrhini, Hominidae,
Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
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Inoue S., Yoshida S., Urakawa I., Mizutani S., Okazaki H.;
Inoue S., Yoshida S., Urakawa I., Mizutani S., Okazaki H.;
Submitted G., Protein coupled receptor.";
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
--- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
--- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
EMBL, AB041940; BAD835941; -; mRNA.
                                                                                                                                                                                                                                                                             Cytoplasmic (Potential).
Vlinked (GlCNAc. . .) (Potential)
N-linked (GlCNAc. . .) (Potential)
By similarity.
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 Glycoprotein; Receptor; Transducer;
                                                                                                                                                                                                                                                                                                                                                                                  Score 1124; DB 1; Length 307; Pred. No. 3e-76; 30; Mismatches 51; Indels
                                                                  Cytoplasmic (Potential).
2 (Potential).
2 (Potential).
3 (Potential).
Cytoplasmic (Potential).
4 (Potential).
Extracellular (Potential).
                                                                                                                                                                                                                            6 (Potential).
Extracellular (Potential)
7 (Potential).
                                                                                                                                                                                                                                                                                                                                                   0B3D02CECB16710D CRC64;
                                    Extracellular (Potential)
                                                                                                                                                                                           5 (Potential).
Cytoplasmic (Potential).
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Last annotation update)
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34152 MW;
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       receptor;
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Name=KPG 007;
Homo sapIens (Human).
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QSKU21;
                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 223; Conservative
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     coupled
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                  Transmembrane
TOPO_DOM
     G-protein
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SEQUENCE
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                            .; IEA
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 25, Last annotation update)
Mus musculus adult male bone CDNA, RIKEN full-length enriched library, clone:9830121M19 product:G protein-coupled receptor 35, full insert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GPYLPLAVVVPCSLKVVTALAQRPPTDVGQABATRKAARMVWANLLVFVVCFLPLHVGLT
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sclurognathi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MNGTYNTCGSSDLTWPPAIXLGFYAYLGVLLVLGLLLNSLALMVFCCRMQQWTETRIYMT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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STRAINECSTBL/60; TISSUE-Bone;
MEDLINE-21085660; Pubmed-11217851; DOI=10.1038/35055500;
Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
                                                                                                                                                                                                                 PEAM; PF00001; 7tm 1; 1.

PRINTS; PR01237; GPCRHODOPSN.

PROSITE; PS00237; G PROTEIN RECEP F1_1; 1.

PROSITE; PS50262; G PROTEIN RECEP F1_2; 1.

G-profein coupled receptor; Receptor; Transmembrane.

G-profein 307 AA; 34152 MW; 0B3D02CECB16710D CRC64;
GO, GO:0016021; C:integral to membrane; IEA.
GO, GO:0045028; P:purinergic nucleotide receptor activity, G-.
GO; GO:004872; F:receptor activity; IEA.
GO; GO:0001884; P:rhodopsin-like receptor activity; IEA.
GO; GO:0001884; P:rhodopsin-like receptor protein signalin.
GO; GO:0007165; P:signal transduction; IEA.
InterPro; IPR00226; GPCR_Rhodopsn.
InterPro; IPR002286; P2_purnocptor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                               69.6%; Score 1124; DB 2
71.9%; Pred. No. 3e-76;
iive 30; Mismatches 5
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A Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Gojobori T., Bono H., Ksaukwa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Bakai K., Okido T., Puruno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Blake J., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringawald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Whittaker C., Willming L., Wanshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The FANTOM Consortium, the RIKEN Genome Exploration Research Group Phase I & II Team; "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=C57BL/63; TISSUE=Bone;
MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Komo H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length CDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000).
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MRDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
Konno H., Akiyama J., Nishi K., Nagaoka T., Tashiro H., Itoh M.,
Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
Yamamoto R., Matemimoto H., Sakaguchi S., Indegami T., Kashiwagi K.,
Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RIKEN integrated sequence analysis (RISA) system-384-format
Sequencing pipeline with 384 multicapillary sequencer.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
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GO; GO:0016021; C:integral to membrane; TAS.
InterPro; IPR000276; GPCR_Rhodpsn.
InterPro; IPR002286; P2_purnocptor.
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STRAIN=C57BL/6J; TISSUE=Bone;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60,770 full-length cDNAs.";
Nature 420:563-573(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hayashizaki Y.;
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InterPro; IPR002286; P2 Pfam; PF00001; 7tm\_1; 1

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | HPLRARGLRSPRQAAAVCAVLWVLVIGSLVARWLLGIQEGGFCFRS-TRHNFNSMRFPLL 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NLAVADLCLLCTLPFVLHSLR-DTSDTPLCQLSQGIYLTNRYMSISLVTAIAVDRYVAVR 119
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TISSUB-Embryonic body between diaphragm region and neck;

MEDLINE-21085660, PubMed=1217851, DOI=10.1038/35055500,

Kawai U., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Fleischmann W., Gasaterland T., Gissi C., King B., Kochiwa H.,

Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
                                                                                                                                                                                                                                                                                                                                                                                   1 MNGTYNTCGSSDLTWPPAIKLGFYAYLGVLLVLGLLLNSLALWVFCCRMQQWTETRIYMT
                                                                                                                                                                                                                                                                                                                                                                                                                               1 MNST--TCNST-LIWPASVNNFFITYSALLLVLGLLLNSVALWVFCYRMHQWTETRIYMT
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TISSUE=Embryonic body between diaphragm region and neck;
MEDLINE=99279253; Pubmed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
                                                                                                                                                                                                                                                                                                                      Gaps
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01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Mus musculus 12 days embryo embryonic body between diaphragm region and neck cDNA, RIXEN full-length enriched library, clone:9430051L15
product:G protein-coupled receptor 35, full insert sequence.
                                                                                                                                                Transmembrane
                                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                          Query Match 69.6%; Score 1123; DB 2; Length 307; Best Local Similarity 71.9%; Pred. No. 3.6e-76; Matches 223; Conservative 30; Mismatches 51; Indels
PRINTS; PR00237; GPCRRHODOPSN.
PRINTS; PR01157; P2YPUNNOCPTR.
PROSITE; PS00237; G PROTEIN RECEP_F1_1; 1.
PROSITE; PS0262; G PROTEIN RECEP_F1_2; 1.
G-protein coupled receptor; Receptor; Trans SEQUENCE 307 AA; 34140 MW; 8EB439AAED5F7656 CRC64;
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"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
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01-MAR.2003 (TrEMBLrel. 23, Last seq
01-OCT-2003 (TrEMBLrel. 25, Last ann
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QBBS98_MOUSE PRELIMINARY;
QBBS98;
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TISSUB-Embryonic body between diaphragm region and neck;
A dachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
A budda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
A Hayashida K., Hayatsu W., Hiraoka T., Hiraoka T., Hirozane T.,
A Hori P., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
A Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M., Mishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
A saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tagami M.,
Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
Subitted (JUL-2011) to the EMBL/GenBank/DDB databases
C. I- SIMILAKIY: Belongs to the G-protein coupled receptor I family.
REBIL AKOSATON.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUB=Embryonic body between diaphragm region and neck;

TISSUB=Embryonic body between diaphragm region and neck;

TISSUB=Embryonic body between diaphragm region and neck;

Shibata K., Itoh M., Alzawa K., Nagaoka S., Sasaki N., Carninci P.,

Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,

A Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,

Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,

Pujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watshiki M.,

A Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,

RIKEN integrated sequence analysis (RISA) system-384-format

Genome Res. 10:1757-1771 (2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE-Embryonic body between diaphragm region and neck;
MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000).
Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustinnich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Masaiman J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyo-oka K., Wang K.H., Wavitz C., Whittaker C., Wilming L., Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                      the RIKEN Genome Exploration Research Group Phase I & II Team, "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."; Nature 420:563-573(2002).
                                                                                                                                                                                                                                              "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                         STRAIN=CS7BL/6J;
TISSUE=Embryonic body between diaphragm region and neck;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MGI; MGI:1929509; Gpr35.
GO; GO:0016021; C:integral to membrane; TAS.
InterPro; IPR00276; GPCR_Rhodpsn.
InterPro; IPR002286; P2_purnocptor.
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PRINTS; PR01157; P2YPURNOCPTR.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
                                                                                                                                                                                                                                                                      Nature 409:685-690(2001).
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NUCLECTIDE SEQUENCE.

NUCLECTIDE SEQUENCE.

NUCLECTIDE SEQUENCE.

NUCLECTION O., AURY J.M., Fischer C., Ozouf-Costaz C., Bernot A.,

Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,

Nathouard V., Jubin C., Castelli V., Ratinka M., Vacherie B.,

Anthouard V., Jubin C., Castelli V., Ratinka M., Vacherie B.,

Anthouard V., Salli Z., Cattolico L., Poulain J., De Berardinis V.,

Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,

Arard G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,

Kellis M., Volff JN., Guigo R., Zody M.C., Mesirov J.,

Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,

Landet V., Schachter V., Weissenbach J., Roset Crollius H.,

"Genome duplication in the teleost fish Tetraodon nigroviridis reveals
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                                                                                                                                                                                                                                            1 MNGTYNTCGSSDLTWPPAIKLGFYAYLGVLLVLGLLLNSLALWVFCCRMQQWTETRIYMT
                                                                                                                                                                                                                                                                                                        1 MNST--TCNST-LTWPASVNNFFIIYSALLLVLGLLLNSVALWVFCYRMHQWTETRIYMT
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Genoscope, Whitehead Institute Centre for Genome Research,
Genoscope, Whitehead Institute Centre for Genome Research,
Submitted (FBB-2004) to the EMBL/GenBank/DDBJ databases.
I- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DBBJ whole genome shotgun (WGS) entry which is
preliminary data.
I- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
                                                                                                                                                                                   Gaps
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13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
13-SEP-2005 (Fragment)
13-SEP-2005 (TrEMBLrel)
13-SEP-2
                                  Transmembrane
                                                                                                                                                                                   ;
9
                                                                                                              / Match 68.7%; Score 1109; DB 2; Length 307; Local Similarity 71.3%; Pred. No. 4e-75; nes 221; Conservative 30; Mismatches 53; Indels e
                                                           CRC64;
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Receptor; Transducer;
SEQUENCE 307 AA; 34260 MW; 923D02CECB0D70AC CR
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Nature 431:946-957(2004).
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Q4TAHO;
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Name=GPR23; Synonyms=P2RY9;
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MEDLINE=22386257; PubMeda12477932; DOI=10.1073/pnas.242603899;

A Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,

A Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

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A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McKwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

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Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
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Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
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-i- SIMILARITY: Belongs to the G-protein coupled receptor 1 family. Bellongs to the G-protein coupled receptor 1 family. InterPro; IPR000276; GPGR Rhodpsn. InterPro; IPR002188; P2Y5_purnocptor.
                                                                                          Pfam; PF00001; 7tm 1; 1.

PRINTS; PR00237; GPCRRHODOPSN.

PRINTS; PR01067; P2YSORPHARR.

PROBITE; PS037; GPROTEIN RECEP F1 1; 1.

PROSITE; PS050262; G PROTEIN RECEP F1 2; 1.

G-protein coupled receptor; Receptor; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                   33;
                                                                                                                                                                                                                                                                                                                 25.9%; Score 417.5; DB 2; Length 305; 34.6%; Pred. No. 2.4e-23; ive 59; Mismatches 108; Indels 33
                                                                                                                                                                                                                                                                    305 AA; 34283 MW; E9F740AD3FF04F32 CRC64;
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13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
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Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           82 -DTSDTPLCQLSQGIYLTNRYMSISLVTAIAVDRYVAVRHPLRARGLRSPRQAAAVCAVL
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25 AYLGVLLVLGLLLNSLALWVFCCRMQQWTETRIYMTNLAVADLCLLCTLPF-VLHSLR--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
-1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
-1- SUBCELLULAR Belongs to the G-protein coupled receptor 1 family.
EMBL; BC095538; Ash95538.1; -; mRNA.
Ensembl; ENSG0000147145; Homo sapiens.
InterPro; IPR000276; GPCR Rhodpsn.
InterPro; IPR000218; P2Y5_purnocptor.
Pfam, PF00001; 7tm_1; 1.
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MEDLINE=97225799; PubMed=9073069; DOI=10.1016/S0378-1119(96)00722-6;
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PRINTS; PRO1067; P2Y5ORPHANR.
PROSITE; PS00237; G PROTEIN RECEP F1 1; 1.
PROSITE; PS0262; G PROTEIN RECEP F1 2; 1.
G-procein coupled receptor; Receptor; Transducer; Trans SEQUENCE 370 AA; 41881 MW; 38267561B1029E48 CRC64;
                                                                                                                                                                                                            and mouse cDNA sequences."; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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TISSUE=G-protein coupled receptors;
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ROUGELIES SEQUENCE LEAVES STATES STATES SEAVERS.

REAGES W.T., GRETHAM D.V., CORTER A.M. SCHOER S., WOLDAY K., MULTUR B. PUBMEGE-15772651; DOI 10138/INARU-CORTER A.M. SCHOER S., SCHOER S., SCHORE S., MULTER R., WEND D., SCOTT C.B., SCHORE S., SCHORE S., SCHORE S., SCOTT G., SCHORE S., SCOTT G., 
O'Dowd B.F., Nguyen T., Jung B.P., Marchese A., Cheng R., Heng H.H.Q., Kolakowski L.F. Jr., Lynch K.R., George S.R.; "Cloning and chromosomal mapping of four putative novel human G-protein-coupled receptor genes."; Gene 187:75-81(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=97366605; PubMed=9223435; DOI=10.1006/bbrc.1997.6895; Janssens R., Boeynaems J.M., Godart M., Communi D.; "Cloning of a human heptahelical receptor closely related to the P2Y5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (www.cdna.org).";
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Kopatz S.A., Aronstam R.S., Sharma S.V.;
"CDNA clones of human proteins involved in signal transduction sequenced by the Guthrie CDNA resource center (www.cdna.org).",
                                                                                                                                                                                                                                                                                                   Bohm S.K., Khitin L.M., Payan D.P., Bunnett N.W.;
Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.
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ROUTECOTIDE SEQUENCE [LARGE SCALE MENA].

RC TISSUE=Brain;

RY NUCLECOTIDE SEQUENCE [LARGE SCALE MENA].

REDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg N.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA HOPKINS R.F., Jordan H., Moore T., Max S.L., Wang J., High F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Glibs R.A.,

RA Niting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

RA "Generation and initial analysis of more than 15,000 full-length human property and mounted analysis of more than 15,000 full-length human property and manalysis of more than 15,000 full-length human property and manalysis of more than 15,000 full-length human property and manalysis of more than 15,000 full-length human property and manalysis of more than 15,000 full-length human property and manalysis of more than 15,000 full-length manalysis of more than 15,000 full
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SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
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-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- TISSUE SPECIFICITY: Not detected in the brain regions thalamus, putamen, caudate, frontal cortex, pons, hypothalamus and
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PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Glycoprotein; Receptor; Transducer; Transmembrane.
Zorilla S., Buck D., Reinhardt R., Poustka A., Rosenthal A., Lehrach H., Meindl A., Minx P.J., Hillier L.W., Willard H.F., Wilson R.K., Waterston R.H., Rice C.M., Vaudin M., Coulson A., Nelson D.L., Weinstock G., Sulston J.E., Durbin R., Hubbard T., Gibbs R.A., Beck S., Rogers J., Bentley D.R.; The DNA sequence of the human X chromosome.";
Nature 434:325-337(2005).
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EMBL, U90323; AAB62087.1; -; Genomic_DNA.
EMBL; U90322; AAB62088.1; -; mRNA.
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PRINTS; PR00237; GPCRHODOPSN.
PRINTS; PR01067; P2X5ORPHANR.
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TISSUE=PCR rescued clones,
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
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TISSUE=PCR rescued clones;

TISSUE=PCR rescued clones;

TISSUE=PCR rescued clones;

MEDLINE=22389257; PubMed=12477932, DOI=10.1073/pnas.242603899;

Strausherg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Altschul S.P., Zeeberg B., Wagner L., Shemmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abrameon R.D., Mallaby S.J.,

Bosak S.A., McKwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
                                                                                                                                                                                                                                                                                                                                                                                                     25 AYLGVLLVLGLLINSLALMVPCCRMQQMTETRIYMTNLAVADLCLLCTLPF-VLHSLR--
                                                       S (Potential).
Cytoplasmic (Potential).
G (Potential).
Extracellular (Potential).
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Cytoplasmic (Potential).
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N-linked (GlcNAc. .) (Potential).
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                     4 (Potential).
Extracellular (Potential)
   (Potential)
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
G protein-coupled receptor 23.
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   Homo sapiens (Human)
 NCBI_TaxID=9606;
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44 AVYSVAFILGLITNSVSLFVFCFRMKNRSETAIFITNLAVSDLLFVCTLPFKIFYNFNHH 103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LISOUGETOR MGC Project,
Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.
Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.
C. -1 SUBGELLUIA ELOCATION: Innegaral membrane protein (By similarity).
REMBL; BCOG69966, AAMS0996.1; -; mRNA.
DR GO; GO:00045021; C:integral to membrane; IEA.
DR GO; GO:00045021; F:receptor activity; IEA.
DR GO; GO:0001584; F:purinargic nucleotide receptor activity, G-. .; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0001159; P:rhodopsin-like receptor protein signalin. .; IEA.
DR GO; GO:0001155; P:signal transduction; IEA.
DR InterPro; IPRO02189; P2Y5_Durnocptor.
DR InterPro; IPRO02189; P2Y5_Durnocptor.
DR PRINTS; PRO10219; P2Y5ORPHANR.
DR PRINTS; PRO10217; GPCRRHODOFSN.
DR PRINTS; PRO10217; GPCRRHODOFSN.
DR PROSITE; PSGO237; GPROTEIN RECEP_F1_1; UNKNOWN_1.
DR PROSITE; PSGO323; GPROTEIN RECEP_F1_2; 1.
KW G-protein coupled receptor; Receptor; Transmembrane.
SQ SEQUENCE 370 AA; 41867 MM; 2AB4B3FFPF813 CRC64;
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield X.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
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QBEKKI;
QBEKKI;
O1-MAR-2003 (TrEWBLrel. 23, Created)
O1-MAR-2004 (TrEWBLrel. 24, Last sequence update)
O1-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Mus musculus 12 days embryo spinal ganglion cDNA, RIKEN full-length
enriched library, clone:D130067812 product:P2Y PURINOCEPTOR 9, full
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 370;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 24.8%; Score 400; DB 2; Length 37 Best Local Similarity 34.1%; Pred. No. 5.8e-22; Matches 103; Conservative 59; Mismatches 112; Indels
                                                                                                                                                                                                                                                                                                                                                                                                   and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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Hayashizaki Y.; "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                          STRAIN=C57BL/6J; TISSUE=Spinal ganglion;
                                                                                                                                Nature 409:685-690(2001).
            Muridae, Murinae; Mus.
                                                                                                                                              The FANTOM Consortium,
                                                                                                                                                                                                                                                       NUCLEOTIDE SEQUENCE
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                                                                                                                                                                    NUCLEOTIDE SEQUENCE
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                        NUCLEOTIDE SEQUENCE
                                                 NUCLEOTIDE SEQUENCE
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63 AVADICILCTLPF-VLHSLR---DTSDTPLCQLSQGIYLTNRYMSISLVTAIAVDRYVAV 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       170 FNSMR--PPLLGFYLPLAVVVFCSLKVVTALAQRPPTDVGQAEAT-RKAARMVWANLLVF 226
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GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:00165028; F:purinergic nucleotide receptor activity, G-. .; IEA.

GO; GO:0004872; F:receptor activity; IEA.

GO; GO:0001884; F:rhodopsin-like receptor activity; IEA.

GO; GO:0007186; F:G-protein coupled receptor protein signalin. .; IEA.

GO; GO:0007165; F:signal transduction; IEA.

InterPro; IPR00276; GPCR Rhodopsn.

InterPro; IPR002188; P2Y5_purnocptor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Murinae; Mus.
Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T., Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T., Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S., Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M., Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H., Santo B., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tanaka Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T., Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.; Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.

- Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.

- Subscributar Location Integral membrane protein (By similarity).
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01-MAR-2004 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Mus musculus 9.5 days embryo parthenogenote cDNA, RIXEN full-length
enriched library, clone:Bl30055Ll5 product:P2Y PURINOCEPTOR 9, full
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
G_protein coupled receptor; Pransducer; Transmembrane.
SEQUENCE 370 AA; 41956 MW; AB126B42343AE6E1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24.8%; Score 400; DB 2; Length 370 34.3%; Pred. No. 5.8e-22; Live 59; Mismatches 112; Indels
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PRINTS; PR00237; GPCRRHODOPSN.
PRINTS; PR01067; P2Y5ORPHANR.
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Matches 104; Conservative
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QBELG2 MOUSE PRELIMINARY;
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Name=Gpr23;
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NEDLINE-CSTBL/62; TISSTE-Spinal ganglion;

NEDLINE-CSTBL/62; TISSTE-Spinal ganglion;

NEDLINE-CSTBL/62; TISSTE-Spinal ganglion;

NEDLINE-CSTBL/62; PubMed=11217851; DOI=10.1038/35055500;

NEDLINE-CSTBL/62; Shinagawa A., Shibata K., Yoshino M., Adachi J., Fukuda S., Arakawa T., Hara A., Pukunishi Y., Konno H., Adachi J., Fukuda S., Anabata T., Rondo S., Yamanaka I., Saito T., Okazaki Y., Gojobri T., Bono H., Kaukawa T., Saito R., Ashburner M., Batalov S., Casavant T., Na Pleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Kuchl P., Lewis S., Marsuo Y., Nikaido I., Pesole G., Quackenbush J., Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Bakai K., Okido T., Furuno M., Aono H., Baddarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldoi M., Bronstein M.J., Bult C., Pletcher C., Fulita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Nordone P., Marchionni L., Mashima J., Mazzarelli J., Mombarts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Saroki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Whithaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohteuki S., Nanabali Y., Yasahi Y., Yawashi, Y., Yanashi Y., Yawashi, Y., Yawashi, Y., Yanashi Y., Yawashi, Y., Yanashi Y., Yawashi, Y., Yanashi Y., Yawashi, Yawashi, Y., Yawashi, Y., Yawashi, Y., Yawashi, Y., Yawashi, Y., Yawashi, Y., Yawashi, Yawa
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MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
Carninci P., Shibata Y., Hayatsu N., Sagahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramateu M., Hayashizaki Y.;
"Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000).
                                                                                   Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                STRAIN=CSTBL/6J; TISSUE=Spinal ganglion; MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9; Carninci P., Hayashizaki Y.; Carninci P., Hayashizaki Y.; High-efficiency full-length cDNA cloning."; Meth. Enzymol. 303:19-44(1999).
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Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
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62 81

28; Gaps

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Search completed: February 9, 2006, 01:00:17
Job time : 168.5 secs
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STRAIN-C57BL/64; TISSUE-Parthenogenote;

MEDLINE=21085660; PubMed=11217851; DOI=10.1038/3505500;

A Arakawa T., Shibata K., Yoshino M., Itoh M., Ishii Y.,

A Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Phudua S.,

A Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

Salto T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Pleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Pleischmann W., Gaasterland T., Nikaido I., Pesole G., Quackenbush J.,

Schriml L.M., Staubli F., Suzuki R., Tomita M., Magner L., Washio T.,

Bakai K., Okido T., Puruno M., Aono H., Baldarelli R., Barsh G.,

Brownstein M.J., Bult C., Pletcher C., Fullita M., Gariboldi M.,

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Norone P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

Nordone P., Rang B., Ringwald M., Rodriguez I., Sakamoto N.,

Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

Wynshaw-Booris A., Yoshida K., Hasesgawa Y., Kawaji H., Kohtsuki S.,

Havashizaki V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUCLECTIDE SEQUENCE.
STRAIN-SCYBL/61/ IISSUE-Parthenogenote;
The PANTOM Consortium.
The RIKEN Genome Exploration Research Group Phase I & II Team,
the RIKEN Genome Exploration Research Group Phase I & II Team,
40.01/10/ Fill-length cunse transcriptome based on functional annotation of
60,770 full-length cunse.
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STRAINE-2791-67, TISSUE-Parthenogenote;
MEDLINE-20499374; PubMed=11042159; DOI=10.1101/gr.145100;
MEDLINE-20499374; PubMed=11042159; DOI=10.1101/gr.145100;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
"Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA lhzaries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUCLEOTIDE SEQUENCE.
STRAIN-C57BL/6J; TISSUE-Parthenogenote;
Adachi J., Aizawa K., Akimura T., Azakawa T., Bono H., Carninci P., Adachi J., Aizawa K., Hamura T., Hara A., Hashizume W., Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T., Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T., Kayashida K., Ishii Y., Itoh M., Kagawa I., Kasukawa T., Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S., Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
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Shibata K., Itoh M., Azawa K., Nagaoka S., Sasaki N., Carninci P.,
Shibata K., Itoh M., Azawa K., Nagaoka S., Sasaki N., Carninci P.,
Sumi N., Itoh I., Nakamura S., Hazama M., Nishine T., Harada A.,
Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kahliwagi K.,
Fujiwake S., Inoue K., Togawa K., Tawa M., Ohara B., Watahiki M.,
Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RISHIKAWA T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RISHIKAWA T., Osawa K., Tanaka T., Matsuura S., Kawai J.,
RISHIMAMA T., Osawa K., Rish A., Hayashizaki Y.;
RISHIMAMA T., Osawa K., Rish A., Hayashizaki Y.;
RISHIMAMA T., Osawa K., Rish A., Hayashizaki Y.;
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Roberski Y., Mutamatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RISHIMAMA T., Osawa K., Tanaka T., Matsuura S., Kawai J.,
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RISHIMAMA T., Osawa K., Tanaka T., Matsuura S., Kawai J.,
RISHIMAMA T., Osawa K., Tanaka T., Matsuura S., Kawai J.,
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RISHIMAMA T., Osawa K., Tanaka T., Matsuura S., Kawai J.,
RISHIMAMA T., Osawa K., Tanaka T., Matsuura S., Kawai J.,
RISHIMAMA T., Osawa K., Tanaka T., Matsuura S., Kawai J.,
RISHIMAMA T., Tanaka T., Matsuura S., Kawai J.,
RISHIMAMA T., Matsuura S., Kawai J.,
RISHIM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Functional annotation of a full-length mouse cDNA collection.";
                                                                                  STRAIN-C57BL/6J; TISSUE-Parthenogenote;
                                                                                                                                                                                            Meth. Bnzymol. 303:19-44(1999).
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NCBI_TaxID=10090,
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Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
A. Togawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases
I. Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases
I. Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases
IN SUBSELLULAR LOCATION: Integral membrane protein (By similarity).
EMBL; AKO45289; BAC32299.1; -; mANA.
EMBL; AKO45289; BAC32299; Mus musculus.
B. MOI; MOI-102384; F:purinergic nucleotide receptor activity, G-. .,; IEA.
GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
GO; GO:0001158; P:rhodopsin-like receptor activity; IEA.
GO; GO:0001165; P:signal transduction; IEA.
B. MOI GO:0001165; P:signal transduction; IEA.
B. InterPro; IPR00278; GPCR_Rhodopsn.
InterPro; IPR002188; P275_purnocptor.
B. Pfam; PP0001; 7tm 1.1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PRO0237; GFCRHODOPSN.
PRINTS; PRO1067; P2Y5ORPHANR.
PROSTITS; P801067; P2Y5ORPHANR.
PROSTITS; P8050263; G PROTEIN RECEP F1 1; UNKNOWN 1.
PROSTITS; P850262; G PROTEIN RECEP F1 2; 1.
G-protein coupled receptor; Receptor; Transducer; Transmembrane.
SEQUENCE 370 AA; 41872 MM; 084C79FEDFD32050 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22;
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34.5%; Pred. No. 2.38-21;
tive 59; Mismatches 103; Indels
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Matches
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GenCore version 5.1.7 (c) 1993 - 2006 Biocceleration Ltd.
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- protein search, using sw model protein ð

; Search time 214.5 Seconds (without alignments) 632.951 Million cell updates/sec 9, 2006, 00:47:19 Pebruary Run on:

US-10-083-168-85 1615 1 MNGTYNTCGSSDLTWPPAIK......AVAPRAKAHKSQDSLCVTLA 309 Title: Perfect score:

Scoring table: Sequence:

2443163 segs, 439378781 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched: 2443163 Total number of hits satisfying chosen parameters:

length: 0 length: 2000000000 Minimum DB seq Maximum DB seq

summaries Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 sm

geneseqp2000s:\* geneseqp2001s:\* geneseqp2002s:\* geneseqp2003as:\* geneseqp2004s:\* geneseqp2005s:\* geneseqp1980s:\* geneseqp1990s:\* A Geneseq 21:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

|   | Description           | Abg95172 Human GPC | Human    | Abg95159 Human GPC | Abp82002 Human G p | Adb67656 Human G p | Ado29394 Human GPC | Ado78094 Human GPR | Human    | Aeb15039 Human GPR |          | Adf70461 Orphan re |          | Aay58645 Human G-p | Human    | Ado78095 Human GPR | Adr10454 Human pro | Adp29765 Human sec | Ado29395 Mouse GPC | Human    | Human    | Abg73513 Human p2y | -        | Human    | Adf91778 Human P2Y |
|---|-----------------------|--------------------|----------|--------------------|--------------------|--------------------|--------------------|--------------------|----------|--------------------|----------|--------------------|----------|--------------------|----------|--------------------|--------------------|--------------------|--------------------|----------|----------|--------------------|----------|----------|--------------------|
|   | ΩI                    | ABG95172           | AAY79576 | ABG95159           | ABP82002           | ADB67656           | AD029394           | AD078094           | ADV73203 | AEB15039           | AAY69989 | ADF70461           | ADF50511 | AAY58645           | ADA84069 | AD078095           | ADR10454           | ADP29765           | AD029395           | AAW62597 | ABP61511 | ABG73513           | ABP81870 | ADH69286 | ADF91778           |
|   | 03                    | 2                  | m        | Ŋ                  | 9                  | 7                  | œ                  | 8                  | σ        | σ                  | ო        | 7                  | 7        | m                  | ø        | œ                  | æ                  | 80                 | 8                  | ~        | Ŋ        | 9                  | 9        | ,        | ω                  |
|   | Query<br>Match Length | 309                | 309      | 309                | 309                | 309                | 309                | 309                | 309      | 309                | 309      | 547                | 309      | 309                | 309      | 394                | 394                | 286                | 307                | 370      | 370      | 370                | 370      | 370      | 370                |
| æ | Query                 | 100.0              | 99.6     | 9.66               | 99.6               | 93.6               | 99.6               | 99.6               | 99.6     | 99.6               | 99.3     | 99.3               | 99.1     | 98.9               | 98.9     | 98.9               | 98.9               | 85.3               | 69.5               | 24.8     | 24.8     | 24.8               | 24.8     | 24.8     | 24.8               |
|   | Score                 | 1615               | 1609     | 1609               | 1609               | 1609               | 1609               | 1609               | 1609     | 1609               | 1603     | 1603               | 1601     | 1597               | 1597     | 1597               | 1597               | 1377               | 1123               | 401      | 401      | 401                | 401      | 401      | 401                |
|   | Result<br>No.         | -                  | 8        | m                  | 4                  | 'n                 | φ                  | 7                  | 60       | σ                  | 10       | 11                 | 12       | 13                 | 14       | 15                 | 16                 | 17                 | 18                 | 19       | 20       | 21                 | 22       | 23       | 24                 |

|                      | Adg81575 Human 1ye<br>Ads84260 Human G p<br>Adv35123 Human tra |   |                      | Human<br>Mouse       | Adw44804 Human RUP<br>Adw44778 Human EFA<br>Aeb20962 Human RUP | Human<br>Human       | Adw44807 Human RUP<br>Adw44802 Human RUP<br>Adw44810 Human RUP<br>Adw44805 Human RUP |
|----------------------|--|---|----------------------|----------------------|--|----------------------|--|
| ADO29049<br>ADQ88244 | ADQ81575<br>ADS84260<br>ADV35123                               | ADF70491<br>ADH69285<br>ADF91777        | ADO29050<br>ABP61510 | ADS84259<br>ADO29415 | ADW44804<br>ADW44778<br>AEB20062                               | ADW44818<br>ADW44796 | ADW44807<br>ADW44802<br>ADW44810<br>ADW44805   |
| 370 8<br>370 8       | 370 8<br>370 8   |   |                      |                      | 363 9  | 363                  | 363 9<br>363 9<br>363 9  |
| 24.8<br>24.8         | 24.8<br>24.8   | 2 | 24.5                 | 24.1<br>24.0         | 23.7   | 73.6<br>73.6<br>73.6 | 23.6<br>23.5<br>23.4<br>23.4   |
| 401                  | 4 4 4<br>4 0 1   | 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4   | 396                  | 389<br>388           | 382.5  | 381.5                | 380.5<br>379.5<br>378.5<br>378.5   |
| 25<br>26             | 28<br>28   | 333                                     | 34                   | 35<br>36             | 38   | 4 4 4<br>2 0 1       | 4 4 4 4<br>G & 4 7   |

## ALIGNMENTS

Human; transmembrane receptor; G-protein coupled receptor; GPCR; allergy; hypertension; reflux disease; depression; migraine; schizophrenia; ulcer; psychotic disorder; asthma; bronchospasm; anaesthesia; myocardial infarction; MI; stroke; glaucoma; anxiety; prostatic hyperplasia; epilepsy; prostate cancer; rhinitis; angina; prostatic hypertrophy; receptor; mutant; mutein. ABG95172 standard; protein; 309 AA. Human GPCR GPR35 mutant A216K. (first entry) 04-DEC-2002 ABG95172; ABG95172 ID ABG RESULT 1 

Homo sapiens Synthetic.

WO200268600-A2.

06-SEP-2002.

26-FEB-2002; 2002WO-US005625.

26-FEB-2001; 2001US-0271913P.

(AREN-) ARENA PHARM INC.

Chalmers DT, Behan DP, Maciejewski-Lenior D, Leonard JN; Liaw CW, Charmer T. Ortuno D;

WPI; 2002-706980/76. N-PSDB; ABS73401 New human G-protein coupled receptor (GPCR), useful for screening agonist or inverse agonist compounds for treating diseases associated with GPCR.

Example 2; Page 189-190; 201pp; English.

The present invention relates to transmembrane receptors, particularly endogenous human G-protein coupled receptors (GPCRs), mutant (non-endogenous) versions of the GPCRs, and the polynuclectide sequences encoding them. The GPCRs are useful for screening agonist or inverse agonist compounds for treating diseases associated with GPCR. Diseases that can be treated with such compounds include allergies, hypertension,

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  reflux disease, depression, migraine, schizophrenia, ulcers, psychotic disorders, asthma, bronchospasm, anaesthesia, myocardial infarction (MI), stroke, glaucoma, prostatic hyperaplasia, epilepsy, prostate cancer, anxiety, prostatic hypertrophy, rhintis, and angina. The present sequence represents a mutant human GPCR
                                                                                                                                                                                                                                                                                                                                                                                                                                      120
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                                                                                                                                                                                                                                                                                                                                 MNGTYNTCGSSDLTWPPAIKLGFYAYLGVLLVLGLLLNSLALWVFCCRMOOWTETRIYMT
                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GPR35; G protein coupled receptor; human; NIDDM1; non-insulin-dependent diabetes mellitus; CAPN10 gene; calpain 10;
                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                       Length 309;
                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                    100.0%; Score 1615; DB 5;
100.0%; Pred. No. 2.6e-168;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note= "encoded by
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Matches 309; Conservative
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                                                                                                                                                                     Sequence 309 AA,
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The present sequence is that of the human gene encoding G protein coupled receptor, GPR35 as deduced from a composite CDNA (see AAA27485). The sequence of GPR35 as deduced from a composite CDNA (see AAA27485). The sequence of GPR35 is similar to that of a putative purinoceptor P279 (34.1% identity) suggesting that AFP or other nuclectide is its ligand. GPR35 mRNA was detected in all adult and foctal tissues examined with relatively higher levels in adult lung, small intestine, colon and stomach. In these tissues, there are 2 major transcripts of 2.4 and 4.4 cm of the GRS5 gene is located in a 49,136 bp region (see AAA2745) within the NIDDMI region of human chromosome 2. This region also includes the CAPN10 gene, which encodes a novel calpain-like cysteine protease, designated calpain 10. Mutations in the CAPN10 gene are responsible for screening for the calpain in a calpain encoding nucleic acid. Methods are also claimed for inclentifying modulators of calpain activity, and using these color insulin secretory response or insulin mediated glucose transport
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                                                                         Method for screening for type 2 diabetes mellitus comprises detecting polymorphism in a calpain encoding nucleic acid segment or a protease-encoding nucleic acid segment.
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Pred. No. 1.2e-167;
0; Mismatches 1;
                                                                                                                                                        Claim 75; Page 237-238; 257pp; English.
            WPI; 2000-339702/29.
N-PSDB; AAA27485, AAY79574, AAY79576.
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Best Local Similarity 99.7%;
Matches 308; Conservative
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Zhou Y, Otani K;

Sreenan S,

oda N,

3, Horikawa Y, Oo Bell GI, Cox NJ;

Polonsky KS, Hanis CL, B

(ARCH-) ARCH DEV CORP. (TEXA ) UNIV OF TEXAS SYSTEM.

99WO-US024890 98US-0105052P 99US-0134175P

21-OCT-1999; 21-OCT-1998; 13-MAY-1999;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        endogenous human G-protein coupled receptors (GPCRs), mutant (non-endogenous) versions of the GPCRs, and the polynucleotide sequences encoding them. The GPCRs are useful for screening agonist or inverse agonist compounds for treating diseases associated with GPCR. Diseases that can be treated with such compounds include allergies, hypertension, reflux disease, depression, migraine, schizophrenia, ulcers, psychotic disorders, astham, bronchospasm, anaesthebesia, myocardial infarction (MI) stroke, glaucoma, prostatic hyperplasia, epilepsy, prostate cancer, anxiety, prostatic hypertensy, thintis, and angina. The present
                                                                                                                                                                                                                                                                                                                                                                       , human G-protein coupled receptor (GPCR), useful for screening agonist inverse agonist compounds for treating diseases associated with GPCR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention relates to transmembrane receptors, particularly
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myocardial infarction; MI; stroke; glaucoma; anxiety;
prostatic hyperplasia; epilepsy; prostate cancer; rhinitis; angina;
prostatic hypertrophy; receptor.
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                                                                                                                                                                                                                                                                        Chalmers DT, Behan DP, Maciejewski-Lenior D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence represents an endogenous human GPCR
                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 29; Page 128-130; 201pp; English.
                                                                                                                                                                       26-FEB-2002; 2002WO-US005625.
                                                                                                                                                                                                       26-FEB-2001; 2001US-0271913P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 99.7
Matches 308; Conservative
                                                                                                                                                                                                                                        (AREN-) ARENA PHARM INC.
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                                                                                                                                                                                                                                                                                         Ortuno D;
                                                                                                                                                                                                                                                                                                                                              N-PSDB; ABS73345.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 309 AA;
                                                                                                      WO200268600-A2.
                                                                        sapiens.
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The present invention describes antigenic peptides (I) comprising: (a) any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino cardida. Also described: (I) an assay for the detection of a particular G protein-coupled receptor (GPCR) or a candidate polypeptide in a sample; and (2) an isolated antibody having high specificity and high affinity or avidity for a particular GPCR. (I) can be used as GPCR modulators and in cantibody against a particular GPCR, and in the production of specific antibody against a particular GPCR, and in the production of specific cantibody against a particular GPCR, and in the production of specific cantibody against a particular GPCR, and in the production of specific cantibodies. The peptides and antibodies are also useful for detecting the consense or absence of corresponding GPCRe. The antigonic peptides for GPCRs and antibodies are useful for diagnosing and designing drugs for creating immune-related disease, immunological-related call proliferative disease, or autoimmune disease, immunological-related call proliferative creaneration-related disease, immunological-related call proliferative disease, or autoimmune disease, e.g. AIDS, Alzheimer's disease, catherosis, bacterial, fungal, protozoan or viral infections. Contentation, allergies, Crohm's disease, diabetes, graft versus host disease, Parkinson's disease, multiple solences's pain, pseriesion, contentation, schizophrenia, dementia, mental retardation, memory contentation renal disorders in which GPCRs are involved. The antibodies may be content in immunoassays and immunodiagnosis. ABZ4521 to antibodies may be contentation in memory and immunoassays and immunodiagnosis. ABZ4552 to antibodies may be contentation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated antigenic peptides e.g., for G protein-coupled receptors (GPCR), useful for diagnosing and designing drugs for treating conditions in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or
                                                                                                                                                          G protein-coupled receptor, GPCR, antigenic peptide; gene therapy; G protein-coupled receptor modulator; antibody, immune-related disease; growth-related disease; cell regeneration-related disease; ALDS, cancer; immunological-related cell proliferative disease; autoimmune disease; Alzheimer's disease, atherosclerosis; infection; osteoarthritis; allergy; osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes; graft versus host disease; Parkinson's disease; multiple sclerosis; pain; psorlasis; anxiety; depression; schizophrenia; dementia; memory loss; mental retardation; spliepy; asthma; tuberculosis; obesity; nausea; hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           used in immunoassays and immunodiagnosis. AB442523 to AB242869 end. GPCR proteins given in ABP81675 to ABP82018, which are used in the exemplification of the present invention
                                                                                                                   Human G protein-coupled receptor GPR35 protein SEQ ID NO:492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure, Fig 1, 523pp, English.
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                                                                      (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
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                       ABP82002;
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Length 309;

Score 1609; DB 6; Pred. No. 1.2e-167;

99.68;

Query Match Best Local Similarity

ABP82002 standard; protein; 309 AA.

99.78;

셤 ŝ 셤 ठे 요 ሯ 셤 & 셤 ઠે 셤

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308; Conservative
      Best Local Similarity
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                                                                                                                                                                                                          61 NIAVADLCILCTLPFVILHSLRDTSDTPLCQLSQGTYLTNRYMSISLVTAIAVDRYVAVRH 120
                                                                                                                                                                                                                                                                                               180
                                                                                                                                                                            61 NLAVADLCLLCTLPFVLHSLRDTSDTPLCQLSQGIYLTNRYMSISLVTAIAVDRYVAVRH 120
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                                                                                                                                                                                                                                                                                            PLRARGLRS PROAAAVCAVLWILVIGSLVARWILGIOEGGFCFRSTRHNFNSMRFPLLGF
                                                                                                               MNGTYNTCGSSDLTWPPAIKLGPYAYLGVLLVLGLLLNSLALWVFCCRMQQWTETRIYMT
                                                         1 MNGTYNTCGSSDLTWPPAIKLGFYAYLGVLLVLGLLLNSLALWVFCCRMOOWTETRIYMT
                                                                                                                                                                                                                                                                                                                                181 YLPLAVVVFCSLKVVTALAQRPPTDVGQABATRKAARMVWANLLVFVVCFLPLHVGLTVR
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Nakamaru K;
   1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human G protein-coupled receptor 35, SEQ ID 25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cardiant; Gene therapy; heart failure; human; G protein-coupled receptor 35; receptor.
   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 111-113; 137pp; Japanese.
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15-APR-2002; 2002JP-00112228.
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Matches 308; Conservative
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Length 309;

DB 7;

99.6%; Score 1609;

Sequence 309 AA;

Query Match

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Transgenic mouse; neurological disorder; adrenal gland disorder; transgenic mouse; neurological disorder; adrenal gland disorder; cardiovascular disorder; intestinal disorder; cardiovascular disorder; blood disorder; bened disorder; bene disorder; bone disorder; blood disorder; mutritive disorder; cancer; cint disorder; netabolic disorder; mutritive disorder; cancer; cancer; added disorder; prostate disorder; breast disorder; without disorder; therus disorder; prostate disorder; sells disorder; skin disorder; thyroid disorder; pancreas disorder; spleen disorder; thymus disorder; antiparkinsonian; antimanic; contral nervous system; respiratory; antidiarnhoeic; antidiabetic; virucide; hepatocropic; antibacterial; antidanemic; antiseborrhoeic; wirucide; hepatocropic; antibacterial; antiallergic; antidiabetic; mimunosuppressive; nephrotropic; gene therapy; GPCR modulator; human; mmunosuppressive; nephrotropic; gene therapy; GPCR modulator; human;
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                                                                                                                                                61 NLAVADLCLLCTLPFVLHSLRDTSDTPLCQLSQGIYLTNRYMSISLVTAIAVDRYVAVRH 120
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Zeng H;
                   Indels
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Madisen L, Mcilwain KL, Pavlova MN, Vassilatis D,
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Pred. No. 1.2e-167;
0; Mismatches 1;
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09-APR-2003; 2003US-0461329P.
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N-PSDB; ADO29916.
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Novel mammalian G protein coupled receptors, useful for identifying compounds that modulates diagnosing and treating disease condition associated with GPCR dysfunction e.g. autoimmune diseases, angina pectoris, Parkinson's disease.

Claim 151; SEQ ID NO 496; 542pp; English

The invention relates to human and mouse G protein-coupled receptors (GPCRs) and nucleic acids encoding them. The invention also relates to sequences at least 90% identical to the GPCR proteins and nucleic acids of the inventing preventing or diagnosing diseases of the invention; methods of screening for associated with GPCRs of the invention; methods of screening for compounds useful in the treatment of GPCR-related diseases; a transgenic compounds useful in the treatment of GPCR-related diseases; a transgenic mouse comprising a GPCR gene of the invention; am ouse comprising a GPCR transgene or in an endogenous GPCR gene; cells derived from the transgene or in an endogenous GPCR gene; cells derived a mutation in a different GPCR polymucleotides of the invention. The mutation in the discloses variants of the GPCR polypeptides and vectors comprising a GPCR nucleic acid. The GPCR nucleic acid. Alzheimer's disease, comprising a GPCR nucleic acid. The GPCR nucleic acid. Alzheimer's disease, be used in the disquancis, treatment or prevention of a wide variety of diseases including neurological disorders (e.g., Alzheimer's disease, depression, diabetic neuropathy, Parkinson's disease or schizophrenia); disorders of the color or intestine of syndrome); cardioral disorders (e.g., angina, cardiac arrhythmia or syndrome); cardioral disorders (e.g., angina, cardiac arrhythmia or syndrome); cardiovascular disorders (e.g., angina, cardiac arrhythmia or syndrome); pone and joint disorders (e.g., angina, cardiac arrhythmia or syndrome); pone and joint disorders (e.g., angina, cardiac arrhythmia or aneemia or leukaemia); immunu disorders (e.g., aucidemina disorders (e.g

1 MNGTYNTCGSSDLTWPPAIKLGFYAYLGVLVJGLLLNSLALWVFCCRMQQWTBTRIXMT 61 NLAVADLCLLCTLPFVLHSLRDTSDTPLCQLSQGIYLTNRYMSISLVTAIAVDRYVAVRH 1 MNGTYNTCGSSDLTWPPAIKLGFYAYLGVLLVLGLLLNSLALWVFCCRMQQWTETRIYMT NLAVADLCLLCTLPFVLHSLRDTSDTPLCQLSQGIYLTNRYMSISLVTAIAVDRYVAVRH Gaps ö 99.6%; Score 1609; DB 8; Length 309; 99.7%; Pred. No. 1.2e-167; 1; Indels 0; Mismatches Matches 308; Conservative Query Match Best Local Similarity 61 셤 ò 요 ò

LAVGWNACALLETIRRALYITSKLSDANCCLDAICYYYMAKEFQEASALAVAPRAKAHKS YLPLAVVVFCSLKVVTALAQRPPTDVGQAEATRKAKRMVWANLLVFVVCFLPLHVGLTVR 241 181 181 셤 ò 셤 ò

QDSLCVTLA 309 301

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RESULT 7 ADO78094 ID ADO7

Sequence 309 AA;

9 9

121 PLRARGLRSPRQAAAVCAVLWVLVIGSLVARWILGIQEGGFCFRSTRHNFNSMRFPLLGF

240 

300

ADO78094 standard; protein; 309 AA.

(first entry) 26-AUG-2004 

ADO78094;

Human GPR35

tumour-associated antigen; TAG; cancer; lung cancer; breast cancer; prostate cancer; colon cancer; stomach cancer; pancreatic cancer; ear cancer; nose cancer; throat cancer; kidney cancer; cervical cancer; melanoma; tumour; human; GPR35.

Homo sapiens

DE10254601-A1

03-JUN-2004

22-NOV-2002; 2002DE-01054601.

22-NOV-2002; 2002DE-01054601

(GANY-) GANYMED PHARM AG

Koslowski M; Sahin U, Tuereci O,

WPI; 2004-421820/40. N-PSDB; ADO78086. Composition containing inhibitor of expression or activity of specific tumor-associated antigens, useful for treating cancers, also related compositions for diagnosis and monitoring.

Claim 72; SEQ ID NO 9; 124pp; German

agent that inhibits the expression or activity of a tumour-associated antigen (TAG) that is encoded by a nucleic acid. The pharmaceutical compositions and related compositions, are used for treatment of diseases associated with (abnormal) expression of TAG, specifically cancer e.g. of lung, breast, prostate, colon, stomach, pancreas, ear/nose/throat, kidney or cervix, also melanoma. Compositions containing TAG, or related nucleic acid, antibodies or host cells, are also useful for diagnosis and sequence of a human GPR35. The invention relates to pharmaceutical compositions that comprise an

Sequence 309 AA;

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ö Gaps ö Length 309; Indels ;; Score 1609; DB 8; Pred. No. 1.2e-167; 0; Mismatches 1; 99.6%; Best Local Similarity 99.7 Matches 308; Conservative Query Match

9 1 MNGTYNTCGSSDLTWPPAIKLGFYAYLGVLLVLGLLLNSLALWVFCCRWQQWTFTRIYMT

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120 NLAVADI.CLI.CTL.PFVLHSLRDTSDTPL.CQLSQGIYL.TNRYMSISLVTAIAVDRYVAVRH 61 120

61 NLAVADLCLLCTLPFVLHSLRDTSDTPLCQLSQGIYLTNRYMSISLVTAIAVDRYVAVRH PLRARGLRSPRQAAAVCAVLWVLVIGSLVARWLLGIQEGGFCFRSTRHNFNSMRFPLLGF 121 121 YLPLAVVVFCSLKVVTALAQRPPTDVGQAEATRKAKRMVWANLLVFVVCFLPLHVGLTVR 240 181

301 ODSLCVTLA 309

301 QDSLCVTLA 309

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61 NLAVADLCLLCTLPFVLHSLRDTSDTPLCQLSQGIYLTNRYMSISLVTAIAVDRYVAVRH 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to an antibody immunospecifically binds to p-cadherin or its fragment. The antibody is useful in preparing a composition for treating or preventing a cancer-associated disorder. The present sequence represents the amno acid sequence of a protein upregulated in human colon cancer cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                                                                                               New antibody that immunospecifically binds to p-cadherin, useful in preparing a composition for treating or preventing a cancer-associated disorder.
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                                                                                                                   Human colon tumor cell upregulated protein SEQ ID NO 44.
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99.7%; Pred. No. 1.2e-167;
iive 0; Mismatches 1;
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                           ADV73203 standard, protein, 309 AA.
                                                                                                                                                    cancer; neoplasm; cytostatic.
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Mazzarella RA, Staten NR;
                                                                                      (first entry)
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                                                                                        10-MAR-2005
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                                                         ADV73203;
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LAVGWNACALLETIRRALYITSKISDANCCLDAICYYYMAKEPQRASALAVAPRAKAHKS 300

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241 LAVGWNACALLETIRRALYITSKUSDANCCLDAICYYYMAKEFQEASALAVAPRAKAHKS 300

301 QDSLCVTLA 309

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screening; cardiovascular disease; gastrointestinal disease; liver disease; cancer; neoplasm; metabolic disorder; hematological disease; respiratory disease; inflammation; neurological disease; urological disorder; cardiovascular-gen.; gastrointestinal-gen.; hepatotropic; cytostatic; metabolic; antianemic; respiratory-gen.; antianflammatory; neuroprotective; uropathic; receptor.
                                                                                                                                                                                                                                                                                                                             Screening of therapeutic agents useful in treating specified diseases involves contacting test compound with G-protein coupled receptor GPR35, and detect binding of test compound to polypeptide.
                                                                                                                    G-protein coupled receptor 35; GPR35; G-protein coupled receptor; GPCR;
                                                                                                                                                                                                                                                                                       Ĥ
                                                                                                                                                                                                                                                                                       Geerts A, Summer
                                                                                                                                                                                                                                                                                                                                                               Disclosure, SEQ ID NO 2; 96pp, English.
                                                 AEB15039 standard; protein; 309 AA.
                                                                                                                                                                                                                                    02-DEC-2004; 2004WO-EP013679.
                                                                                                                                                                                                                                                     12-DEC-2003; 2003EP-00028614
                                                                                  08-SEP-2005 (first entry)
                                                                                                                                                                                                                                                                    (FARB ) BAYER HEALTHCARE
                                                                                                                                                                                                                                                                                      Golz S, Brueggemeier U,
                                                                                                   Human GPR35 polypeptide
301 QDSLCVTLA 309
                                                                                                                                                                                                                                                                                                     WPI; 2005-506223/51
                                                                                                                                                                                                                                                                                                              N-PSDB; AEB15038.
                                                                                                                                                                                                   WO2005059546-A2
                                                                                                                                                                                     Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Human receptor-associated protein; HRAP; Incyte clone 3083742; cytostatic; immunomodulatory; antiinflammatory; cardiant; antianaemic; antiartisetica antiartisedicartisedicartisedicartisedicartisedicartisedicartisedicartisedicartisedicartised; antidabetic; dermatological; neuroprotective; diagnosis; treatment; prevention; reproductive disorder; cardiovascular; cell proliferative; autoimmune; inflammatory; allergy; gastrointestinal; atherosclerosis; cirrhosis; leukaemia; cancer; AIDS; arthritis; anaemia; asthma; dermatitis; diabetes; osteoporosis; multiple sclerosis; irritable bowel syndrome.
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                                                                                                                                                                                                       YLPLAVVVFCSLKVVTALAQRPPTDVGQAEATRKAARNVWANILVFVVCFLPLHVGLTVR 240
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                                                                                                                     NLAVADLCLLCTLPFVLHSLRDTSDTPLCQLSQGIYLTNRYMSISLVTAIAVDRYVAVRH 120
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                                                                           MNGTYNTCGSSDLTWPPAIXLGFYAYLGVLLVLGLLLNSLALWVFCCRMQQMTETRIYMT
                                                                                                       NLAVADLCLLCTLPFVLHSLRDTSDTPLCQLSQGIYLTNRYMSISLVTAIAVDRYVAVRH
                                                                                                                                                  PLRARGLRSPROAAAVCAVLWVLVIGSLVARWLLGIQEGGFCFRSTRHNFNSMRFPLLGF
                                                                                                                                                                     121 PLRARGLKSPROAAVCAVLWVLVIGSLVARWLLGIQEGGFCFRSTRHNFNSMRFPLLGF
                                                                                                                                                                                          YLPLAVVVPCSLKVVTALAQRPPTDVGQAEATRKAKRMVWANLLVFVVCFLPLHVGLTVR
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                                                              1 MNGTYNTCGSSDLTWPPAIKLGFYAYLGVLLVLGLLLNSLALWVPCCRMQQWTBTRIYMT
                                          Gaps
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                      Length 309;
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                                          Indels
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238
/note= "Potential phosphorylation site"
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/label= Signature_sequence
/note= "G-protein_coupled_receptor"
                      99.6%; Score 1609; DB 9; 99.7%; Pred. No. 1.2e-167;
                                Pred. No. 1.26
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                           Matches 308; Conservative
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                       Query Match
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The present sequence is human receptor-associated protein (HRAP) from Incyte clone 3083742 obtained from OVARTUN01 cDNA library. This sequence is expressed in haematopoietic/famune, gastrointestinal and reproductive tissues. HRAP has cytostatic, immunomodulatory, antianflammatory, cardiant, antiarteriosclerotic, hepatotropic, antiantentitic, antiateriosclerotic, hepatotropic, antianaemic, antiasthmatic, antiateriosclerotic, neuroprotective activities. The present sequence is useful in the diagnosis, treatment and prevention of disorders associated with HRAP expression, especially cell proliferative, autoimmunefinflammatory, reproductive, cardiovascular and autoimmunefinflammatory, reproductive, cardiovascular and gastrointestinal disorders (e.g. atherosclerosis, cirrhosis, leukaemia, cancer, AIDS, arthritis, allergies, anaemia, asthma, dermatitis, diabetes, osteoporosis, multiple sclerosis and irritable bowel syndrome)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New human receptor-associated proteins (HRAP) useful for the diagnosis, treatment and prevention of cell proliferative, autoimmune, inflammatory, reproductive, cardiovascular, and gastrointestinal disorders.
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  /note= "Potential phosphorylation site"
261
                                                                           /note= "Potential phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                      Tang YT, Gorgone GA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99.3%; Score 1603; DB 3;
99.4%; Pred. No. 5.4e-167;
tive 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 76; 99pp; English.
                                                                                                                                                                                                                                                                                         98US-0160065P.
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                                                                                                                                                                                                                                                                                                                                                                          (INCY-) INCYTE PHARM INC
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                                                                                                                                                                                                                                                                                                                                                                                                                            Hillman JL, Yue H, L
Corley NC, Baughn MR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2000-205710/18.
N-PSDB; AAZ50891.
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                                                                                                                                  WO200008155-A2
Modified-site
                                                    Modified-site
                                                                                                                                                                                                                                          06-AUG-1999;
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                                                                                                                                                                                                                                                                                                                        01-SEP-1998;
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241 LAVGWNACALLETIRRALYITSKLSDANCCLDAICYYYMAKEFQEASALAVAPRAKAHKS 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Endocrine cell lines originated from mammalian hypothalamus and pancreatic islet, applicable in expression cloning systems of bloactive peptide precursor genes, and in screening G protein-coupled receptor ligands.
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                                                                                                                                                                                                                                                                                                                                                                                                          mutant; mutein; transformation; endocrine cell line;
expression cloning system; bioactive peptide; GPCR ligand; human.
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Best Local Similarity 99.4%; Pred. No. 8.9e-167;
Matches 307; Conservative 0; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                           Human GPCR GPR35 D113A mutein (SeqID 191).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-APR-2003; 2003WO-JP004840.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (KYOW ) KYOWA HAKKO KOGYO KK.
                                                                                                                                                                                                                                                                                                               (first entry)
                                                   301 QDSLCVTLA 309
                                                                                               301 ODSLCVTLA 309
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Nishi T, Obinata M;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This invention relates to a novel method of identifying ligands to an orphan receptor protein which comprises transforming cells with DNA encoding a fusion protein of the orphan receptor with a fluorescent protein, so that the fusion protein is expressed in the cells (or cell membranes isolated from them) and contacting the cells with the potential ligand to be tested. A suitable fluorescent protein for incorporation in the fusion protein is green fluorescent protein (GFP), for example GFP-1, wild-type GFP, GFPPU or Enhanced GFP (EGFP). The method is useful for the identification of ligands binding to an orphan receptor protein.
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                                                                                                                                                                                                                                   ligand, orphan receptor protein; fusion protein; fluorescent protein; cell expression; green fluorescent protein; GFP; GFP-1; wild-type GFP; GFPuv; Enhanced GFP; EGFP; human.
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                                                                                                                                                                                       Orphan receptor ligand-related human protein SeqID84.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kawamata Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7
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Pred. No. 1.1e-166;
0; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ogi K, Komatsu H,
                                                 ADF70461 standard; protein; 547 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-FEB-2002; 2002JP-00045728.
23-JUL-2002; 2002JP-00213949.
11-OCT-2002; 2002JP-00298237.
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Best Local Similarity 99.4%;
Matches 307; Conservative (
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                                                                                                                                           (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2003-697654/66
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                                                                                                                                                                                                                                                                                                                                                                                  WO2003071272-A1
                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                           12-FEB-2004
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                                                                                             ADF70461;
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RESULT 11
ADF70461
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Kunitomo H;

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Length 309;

Indels

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us-10-083-168-85.rag

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obesity; anorexia; bulimia; asthma; Parkinson's disease; acute heart
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                                                                                                                     Query Match
Best Local Si
Matches 306;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               puringrgic family of polypeptides and a G-protein coupled receptor. The invention provides GPR35A polypeptides having at least 70% identity with the present sequence, GPR35A polypeptides combinant materials, and methods for their production. GPR35A polypeptides can be used for identifying agonists and antagonists/inhibitors, and for detecting diseases associated with inappropriate GPR35A activity or levels. GPR35A polypeptides and polymucleotides, anoists, antagonists and antibodies are used to treat infections such as bacterial, fungal, protozoan and viral infections, particularly HIV-1 and HIV-2; pain; cancer; diabetes;
                         120
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                                                                                                              240
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                                                                                                                                                                     MNGTYNTCGSSDLTWPPAIKLGFYAYLGVLLVLGLLLNSLALWVFCCRMQQWTETRIYMT 60
                                                                                                                                                                                                                                                                                                                                                                    GPR35A; human; G-protein coupled receptor; purinergic; 7-transmembrane receptor; antibiotic; antifungal; antiviral; analgesic; 7-transmembrane receptor; antibiotic; antianthmatic; antiparkinsonian; hypotensive; hypotensive; osteopathic; antianginal; cardiant; cerebroprotective; antiuleer; antiallergic; antimigraine; antidemetic; tranquillizer; antidepressant; neuroleptic; nootropic; anticonvulsant; therapy; diagnosis; vaccine.
                                                                                NLAVADLCLLCTLPFVLHSLRDTSDTPLCQLSQGIYLTNRYMSISLVTALAVDRYVAVRH
                                                                                                                                  YLPLAVVVPCSLKVVTALAORPPTDVGQAEATRKAARMVWANLLVFVVCFLPLHVGLTVR
                                                                                                                                                        LAVGWNACALLETIRRALYITSKLSDANCCLDAICYYYWAKBFQEASALAVAPRAKAHKS
                                                                                                              YLPLAVVVFCSLKVVTALAQRPPTDVGQAEATRKAKRMVWANLLVFVVCFLPLHVGLTVR
                                                                   PLRARGLRSPRQAAAVCAVLWVLVIGSLVARWLLGIQEGGFCFRSTRHNFNSMRFPLLGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       present sequence represents human GPR35A, a novel member of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New human GPR35A polypeptides and polynucleotides used to identify agonists, antagonists and inhibitors for use in therapy.
                                                                                                                                                                                                                                                                                                                                                 Human G-protein coupled receptor GPR35A.
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                                                                                                                                                                                                                                                                                  AAY58645 standard; protein; 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (SMIK ) SMITHKLINE BEECHAM CORP
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                                                                                                                                                                                                       309
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N-PSDB; AAZ35390.
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failure; hypotension; hypertenation; urinary retention; osteoporosis; angina pectoris; myocardial infarction; stroke; ulcers; allergy; benign prostatic hypertrophy; migraine; vomiting; psychotic and neurological disorders including anxiety, schizophrenia, manic depression, depression, delirium, dementia and severe mental retardation; and dyskinesias such as Huntingdon's or Gilles de la Tourette's syndrome. The polypeptide is also useful for production of vaccines
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           human; marker; expressed sequence tag; EST; arabidopsis; tumour; stress-induced phenotype; hyperosmotic stress; colon cancer; immunogen;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YLPLAVVVFCSLKVVTALAQRPPTDVGQAEATRKAKRMVWANLLVFVVCFLPLHVGLTVR
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                                                                                                                                                                                                                        Length 309;
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                                                                                                                                                                                                                        Score 1597; DB 3;
Pred. No. 2.5e-166;
0; Mismatches 3;
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22-OCT-2001; 2001US-0330457P.
19-FEB-2002; 2002US-0357144P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-MAY-2002; 2002WO-IB004189
                                                                                                                                                                                                                             98.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                 Local Similarity 99.0
les 306; Conservative
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N-PSDB; ADA84068.
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                                                                                                                                                                                      Sequence 309 AA;
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us-10-083-168-85.rag

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The invention relates to a novel method for determining if a nucleic acid is a marker for a predetermined phenotype/cell type of interest from a blological species. The method comprises performing a global comparison of a group of expressed sequence tags (ESTs) known to be expressed in the comparison of a group of expressed sequence tags (ESTs) known to be expressed in the chancype/cell type of interest which all ESTs expressed in the phenotype/cell type of interest with all ESTs expressed in the chancype/cell type of interest is a marker for a predetermined phenotype or cell type of interest from a biological species, preferably arabidopsis or chuman. The cell type of interest is an abnormal cell such as a tumour cell, and the predetermined phenotype is a stress induced phenotype such as hyperosmotic stress or high salt conditions. A method of the invention is also useful for detecting at tumour cell, and for regulating or preventing the growth of a tumour cell, and for regulating or cancer in a human, for detecting a tumour cell, and for regulating or tumour-associated markers. A polypeptide of the invention is useful as an immunogen for vaccinating an animal. The present sequence represents a cumour-associated markers. A polypeptide of the invention is useful as an immunogen for vaccinating an animal. The present sequence represents a cumour-associated markers.
Determining if a nucleic acid is a marker for a phenotype/cell type of interest, by global comparison of expressed sequence tags known to be expressed in the phenotype/cell type with all ESTs expressed in normal tissue.
                                                                                                                                                                               Claim 29; Page 448-449; 516pp; English.
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# Sequence 309 AA;

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181 YLPLAVVVFCSLKVVTALAQRPPTDVGQAEATRKAARWWANLLVFVVCPLPLHVGLTVR 240
                                                                                                       61 NLAVADLCLLCTLPFVLHSLRDTSDTPLCQLSQGIYLTNRYMSISLVTAIAVDRYVAVRH 120
                                                                                                                        61 NLAVADLCLLCTLPFVLHSLRDTSDTPLCQLSQGIYLTNRYMSISLVTALAVDRYVAVRH 120
                                                                                                                                                          121 PLRARGLRSPRQAAAVCAVLWVLVIGSLVARWLLGIQEGGFCFRSTRHNFNSMRFPLLGF 180
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                                                                   1 MNGTYNTCGSSDLTWPPAIRLGFYAYLGVLAVLGLLLNSLALWYFCCRMQQWTETRIYMT
                                                                                                                                                                                                           YLPLAVVVFCSLKVVTALAQRPPTDVGQAEATRKAKRMVMANLLVFVVCFLPLHVGLTVR
                                                      MNGTYNTCGSSDLTWPPAIKLGFYAYLGVLLVLGLLLNSLALWVPCCRMQQWTBTRIYMT
                              Gaps
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     Length 309;
                              3; Indels
   Score 1597; DB 6;
Pred. No. 2.5e-166;
0; Mismatches 3;
     98.94;
Query Match
Best Local Similarity 99.0°
Matches 306; Conservative
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tumour-associated antigen; TAg; cancer; lung cancer; breast cancer; prostete cancer; colon cancer; stomach cancer; pancreatic cancer; ear cancer; nose cancer; throat cancer; kidney cancer; cervical cancer; melanoma; tumour; human; 08735.
                            ADO78095 standard; protein; 394 AA
                                                                                   26-AUG-2004 (first entry)
                                                                                                                Human GPR35 isoform
                                                        ADO78095;
RESULT 15
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The invention relates to pharmaceutical compositions that comprise an agent that inhibits the expression or activity of a tumour-associated antigen (TMg) that is encoded by a nucleic acid. The pharmaceutical compositions and related compositions, are used for treatment of diseases associated with (abnormal) expression of TMg, specifically cancer e.g. of lung, breast, prostate, colon, stomach, pancreas, ear/nose/throat, kidney or cervix, also melanoma. Compositions containing TMg, or related nucleic acid, antibodies or host cells, are also useful for diagnosis and monitoring of tumours. The present sequence represents the amino acid sequence of a human GPR35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 NLAVADLCLLCTLPFVLHSLRDTSDTPLCQLSQGIYLTNRYMSISLVTAIAVDRYVAVRH 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 PLRARGLRSPRQAAAVCAVLWVLVIGSLVARWLLGIQEGGFCFRSTRHNFNSMRPPLLGF 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              266 YLPLAVVVFCSLKVVTALAQRPPTDVGQAEATRKAARMVMANLLVFVVCFLPLHVGLTVR 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LAVGWNACALLETIRRALYITSKLSDANCCLDAICYYYMAKEFQEASALAVAPRAKAHKS 300
                                                                                                                                                                                                                                                                                          Composition containing inhibitor of expression or activity of specific tumor-associated antigens, useful for treating cancers, also related compositions for diagnosis and monitoring.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MNGTYNTCGSSDLTWPPAIKLGFYAYLGVLLVLGLLLNSLALWVFCCRMQOWTETRIYMT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          86 MIGTYNTCGSSDLTWPPAIKLGFYAYLGVLLVLGLLLNSLALWVFCCRWQQWTETRIYMT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  146 NLAVADLCLLCTLPFVLHSLRDTSDTPLCQLSQGIYLTNRYMSISLVTALAVDRYVAVRH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        206 PLRARGLKSPRQAAAVCAVLWVLVIGSLVARWLLGIQEGGFCFRSTRHNFNSWAFPLLGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  326 LAVGWNACALLETIRRALYITSKLSDANCCLDAICYYYMAKEPQEASALAVAPSAKAHKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YLPLAVVVPCSLKVVTALAQRPPTDVGQARATRKAKRMVWANLLVFVVCFLPLHVGLTVR
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Pred. No. 3.3e-166;
0; Mismatches 3;
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                                                                                                                                                                                                                                                                                                                                                                    Claim 72; SEQ ID NO 10; 124pp; German.
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                                                                                                                                                                                                                       Koslowski
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98.98;
                                                                                                           22-NOV-2002; 2002DE-01054601
                                                                                                                                               22-NOV-2002; 2002DE-01054601.
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                                                                                                                                                                                   (GANY-) GANYMED PHARM AG
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Job time: 215.5 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
                                                                                                                                                                                                                                                          WPI; 2004-421820/40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 394 AA;
                                  DE10254601-A1
   Homo sapiens.
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(without alignments)
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(c) 1993 - 2006 Biocceleration Ltd
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1. /GgD2 6/ptodata/1/iaa/5_COMB.pep:*

2. /GgD2 6/ptodata/1/iaa/6_COMB.pep:*

3. /GgD2 6/ptodata/1/iaa/H_COMB.pep:*

4. /GgD2 6/ptodata/1/iaa/PCTUS_COMB.pep:*

5. /GgD2 6/ptodata/1/iaa/RE_COMB.pep:*

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US-09-944-807-21

US-10-314-048A-135

US-08-467-948A-8

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US-08-467-948A-137

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APPLICANT: HORIKAMA, YUKIO

APPLICANT: HORIKAMA, YUKIO

APPLICANT: ODA, NACHISA

APPLICANT: ODA, NACHISA

APPLICANT: CAN, NACH J.

APPLICANT: ZHOU, YUN-PING

APPLICANT: ZHOU, YUN-PING

APPLICANT: ZHOU, YUN-PING

APPLICANT: APPLICANT: CANICHI

APPLICANT: BELL, GRAEME I.

ITILE OF INVENTION: METHODS OF TREATMENT OF TYPE 2 DIABETES

FILE REFERENCE: ARCD:307

CURRENT APPLICATION NUMBER: US/09/422,869

CURRENT FILING DATE: 1999-10-21

SARLIER PILING DATE: 1999-05-13

NUMBER OF SEQ ID NOS: 30

SOFTWARE: PATCHIN VOE: 2.0
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US-10-314-048A-88

US-09-979-603-22

US-09-745-842-16

US-09-745-842-16

US-09-077-173D-2

US-08-148-173D-2

US-08-148-173D-2

US-08-13-9748-372

US-08-13-9748-372

US-08-442-134A-2

US-08-442-134A-2

US-08-442-134A-2

US-08-446-088A-2

US-08-446-088A-3

US-08-749-707-3

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Best Local Similarity 100.0
Matches 309, Conservative
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137, App 157, App 139, App 83, Appl

Sequence Sequence Sequence Sequence Sequence Sequence

S-10-314-048A-24 S-09-979-603-18 S-08-513-974B-374 S-10-314-048A-151

Sequence Sequence Sequence

-09-745-842-15

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APPLICANT: Benan, DOMILIC F.

APPLICANT: Chalmers, Derek T.

APPLICANT: Chalmers, Derek T.

APPLICANT: Learner, Michael

ITILE OF INVENTION: Human G Protein-Coupled Receptors and Modulators Thereof

ITILE OF INVENTION: for the Treatment of Metabolic-Related Disorders

ITILE OF INVENTION: for the Treatment of Metabolic-Related Disorders

ITILE OF INVENTION: for the Treatment of Metabolic-Related Disorders

ITILE OF INVENTION: for the Treatment of Metabolic-Related Disorders

CURRENT APPLICATION NUMBER: US/10/314,048A

CURRENT PILING DATE: 2002-03-12

PRIOR FILING DATE: 2002-03-13

PRIOR FILING DATE: 2002-09-13

PRIOR FILING DATE: 2002-09-13

PRIOR FILING DATE: 2002-09-13

NUMBER OF SEQ ID NOS: 161

SSOTID NO 159
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 213 WSLRQR---QMDRHAKIKRAITFIMVVAIVFVICFLP---SVVVRIRIFWLLHTSGTQNC 266
                          249 --ALLETIRRALY-ITSKLSDANCCLDAICYYYMAKEPQEASALAVAPRAKAHKSQDSLC 305
                                                   281 TNCFLERFAKIMYPITLCLATLNCCFDPPIYYFTLESPQKSFYI-----NAHIRMESLF 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              87 PL----CQLSQGIYLTNRYMSISLVTAIAVDRYVAVRHPLRARGLRSPRQAAAVCAVLWV 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         143 LVIGSLV--ARWLLGIQEGG--FCFR-STRHNF--NSMRFPLLGFYLPLAVVVFCSLKVV 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            34 LGLEFIFGLLGNGLALWIFCFHLKSWKSSRIFLFNLAVADFLLIICLPFLMDNYVRRSDW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 363;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 23.6%; Score 381.5; DB 2;
Best Local Similarity 34.2%; Pred. No. 8.5e-25;
Matches 94; Conservative 48; Mismatches 108;
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                                                                                                                                                                                                                                                                                  Sequence 159, Application US/10314048A Patent No. 6902902 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lowitz, Kevin P.
Behan, Dominic P.
                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Unett, David J.
APPLICANT: Chen, Ruoping
APPLICANT: Richman, Jeremy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Choi, Bryan
Leonard, James
Hakak, Yaron
Liaw, Chen
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dang, Huong T.
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                                                                                                                     306 VT 307
                                                                                                                                                                    335 KT 336
                                                                                                                                                                                                                                                                 JS-10-314-048A-159
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                                                                                                                                                                                              Bequence 2, Application US/08781250
Patent No. 6010877
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Sathe, Genesh
APPLICANT: Wan Horn, Stephanie
APPLICANT: Wan Mao, JOYCe Yue
APPLICANT: Wan Mao, JOYCe Yue
TITLE OF INVENTION: 2
CORRESSONDERCE ADDRESS:
ADDRESSE: GmithKline Beecham
STREET: 709 Swedeland Road
CITT: King of Prussia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              44 AVYSVVPILGLITUSVSLFVFCFRMKARSETAIFITMLAVSDLLFVCTLPFKIFVNFNRH 103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        190 CSLKVVTALAQRPPIDVGQAEAT-RKAARMVWANLLVFVVCFLPLHVGLTVRLAVGWNAC 248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24.9%; Score 402; DB 2; Length 370;
34.1%; Pred. No. 1.6e-26;
tive 60; Mismatches 111; Indels 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PastEM: DOS
SOFTWARE: PastEEG for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,250
CLASSIFICATION: 514
PRIOR APPLICATION: 514
PRIOR APPLICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNOV'.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTOWNEY AGENT INFORMATION:
NAME: William T. Han,
REGISTRATION NUMBER: 34,344
REFRENCE/DOCKET NUMBER: ATGS
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 370 amino acide TYPE: amino acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 34.19
Matches 103; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  // MOLECULE TYPE: protein
U8-08-781-250-2
                                              301 QDSLCVTLA 309
                                                                                             ODSLCVTLA 309
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APPLICANT: Lowitz, Kevin P.
APPLICANT: Lowitz, Kevin P.
APPLICANT: Lowitz, Kevin P.
APPLICANT: Behan, Dominic P.
APPLICANT: Behan, Dominic P.
APPLICANT: Chalmers, Derek T.
APPLICANT: Chalmers, Derek T.
APPLICANT: Lerner, Michael
TITLE OF INVENTION: Human G Protein-Coupled Receptors and Modulators Thereof
TITLE OF INVENTION: for the Treatment of Metabolic-Related Disorders
TITLE OF INVENTION: for the Treatment of Metabolic-Related Disorders
TITLE OF ILLING DATE: 2002-12-06
FILE REFERENCE: 2.016-12-06
FRIOR APPLICATION NUMBER: 09/995,543
FRIOR APPLICATION NUMBER: 09/995,543
FRIOR FILING DATE: 2002-07-29
FRIOR FILING DATE: 2002-07-29
FRIOR FILING DATE: 2002-08-19
FRIOR FILING DATE: 2002-09-13
FRIOR FILING DATE: 2002-09-13
FRIOR PILING DATE: 2002-09-13
FRIOR PILING DATE: 2002-09-13
FRIOR FILING DATE: 2002-09-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   82 DISDIPLOOLSQGIYLINRYMSISLVIAIAVDRYVAVRHPLRARGLRSPRQAAAVCAVLW 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       142 VLVIGSLV--ARWLLGIQEGG--FCFR-STRHNF--NSMRFPLLGFYLPLAVVVFCSLKV 194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ||: ||| |||||||||| || 34 LGLEFIRGIALMIFCFHLKSWKSSRIFLENLAVADFLLICLFFLMDNYVRRWDW 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27 IGVLIVIGILILINSLALWVFCCRMQQWTETRIYMTNIAVADLCLICTLPFVLHSL----R 81
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267 EVYRSVDLAFFITLSFTYMNSMLDPVVYYFSSPSF 301
                                                                                                                                                                                                          Sequence 36, Application US/10314048A
Patent No. 6902902
                                                                                                                                                                                                                                                                                                                      Unett, David J.
Chen, Ruoping
Richman, Jeremy
Connolly, Daniel
Dang, Huong T.
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Leonard, James
Hakak, Yaron
Liaw, Chen
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Best Local Similarity 34.1
Matches 94; Conservative
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Sequence 108, Application US/09170496D Patent No. 6555339

RESULT 5 US-09-170-496D-108

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APPLICANT: Chalmers, Derek T.
APPLICANT: Liaw, Chen W.
TITLE OF INVENTION: No. 6555339-Endogenous, Constitutively Activated Human G Protein-
TITLE OF INVENTION: Receptors
FILE REPERBACE: AREN-0040
CURRENT APPLICATION NUMBER: US/09/170,496D
CURRENT PILING DATE: 1998-10-13
NUMBER OF SEQ ID NOS: 294
SOFTWARE: Patentin version 3.1
SEQ ID NO 108
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Sequence 222, Application US/09170496D

Patent No. 6555339

GENERAL INFORMATION:

APPLICANT: Behan, Dominic P.

APPLICANT: Chalmers, Derek T.

APPLICANT: Liaw, Chen W.

TITLE OF INVENTION: No. 6555339-Endogenous, Constitutively Activated Human G Protein-
TITLE OF INVENTION: Receptors

FILE REFERENCE: AREN-0040

CURRENT APPLICATION NUMBER: US/09/170,496D

CURRENT FILING DATE: 1998-10-13
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; Pred. No. 1.2e-23;
48; Mismatches 105;
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SOFTWARE: Patentin version 3.1
SEQ ID NO 222
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                    APPLICANT: Behan, Dominic P
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; ORGANISM: Homo sapiens
US-09-170-496D-222
                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Homo sapiens
US-09-170-496D-108
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Best Local Similarity
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Best Local Similarity
Matches 94; Conserv
GENERAL INFORMATION:
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Hakak, Yaron
Liaw, Chen
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APPLICANT: Chen, Ruoping
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; ORGANISM: Homo sapiens
US-10-314-048A-135
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US-09-875-076-4
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94 KFGDIPCRLVLFMFAMNRQGSIIFLTVVAVDRYFRVVHPHHALNKISNWTAAIISCLLWG 153
                                        143 LVIG---SLVARWLLGIQEG--GFCFR-STRHNF--NSMRFPLLGFYLPLAVVVFCSLKV 194
                                                                                                                          195 VTALAQRPPTDVGQAEATRKAARMVWANLLVFVVCFLPLHVGLTVRLAVGW-----NA 247
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Patent No. 6773895

GRNERAL INFORMATION

TOTALE OF INVENTION: Method for identifying substances which positively TITLE OF INVENTION: influence inflammatory conditions of chronic TITLE OF INVENTION: inflammatory airway diseases

FILE REPERENCE: 082 0nn

TITLE OF INVENTION: Inflammatory airway diseases

FILE REPERENCE: 082 0nn

FILE REPERENCE: 2001-08-31

PRIOR APPLICATION NUMBER: UK 0021484.1

PRIOR APPLICATION NUMBER: UK 0021484.1

PRIOR APPLICATION NUMBER: UK 0021484.1

NUMBER OF SEQ ID NOS: 24

SOFTWARE: PatentIN Ver. 2.1
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APPLICANT: Unett, David J.
APPLICANT: Chen, Ruoping
APPLICANT: Richman, Jeremy
APPLICANT: Connolly, Daniel
APPLICANT: Connolly, Daniel
APPLICANT: Dang, Huong T.
APPLICANT: Choi, Bryan
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Best Local Similarity
Matches 95; Conserv
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US-09-944-807-21
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LENGTH: 387
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APPLICANT: Liaw, Chem.
APPLICANT: Lowiz, Kevin P.
APPLICANT: Lowiz, Kevin P.
APPLICANT: Behan, Dominic P.
APPLICANT: Chalmers, Derek T.
APPLICANT: Lerner. Michael
TITLE OF INVENTION: Human G Protein-Coupled Receptors and Modulators Thereof
TITLE OF INVENTION: For the Treatment of Metabolic-Related Disorders
TITLE OF INVENTION: For the Treatment of Metabolic-Related Disorders
TITLE OF INVENTION: For the Treatment of Metabolic-Related Disorders
TITLE OF INVENTION: 100 MUBBER: US 100 METABER: US 100 METABER:
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APPLICANT: Liaw, Chen W.

APPLICANT: Liaw, Chen W.

TITLE OF INVENTYON: Human Orphan G Protein Coupled Receptors
FILE REFERENCE: ARENOSO

CURRENT PELLICATION NUMBER: US/09/875,076

CURRENT FILING DATE: 2001-06-06

PRIOR PILLING DATE: 1999-10-12

PRIOR FILING DATE: 1999-10-12

PRIOR PILLING DATE: 60/120,416

PRIOR PILLING DATE: 60/120,416

PRIOR PILLING DATE: 60/120,416

PRIOR PILLING DATE: 60/120,416
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Patent No. 6869776
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INFORMATION FOR SEQ ID NO: 8: SEQUENCE CHARACTERISTICS:
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REGISTRATION NUMBER:
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MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 20005
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                WASHINGTON
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                       US-08-467-948A-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           219 VWANLLVFVVCFLPLHVGLTV----RLAVGWNACALLETIRRALYITSKLSDANCCLDAI 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63 AVADLCLLCTLP----FVLHSLRDTSDTP----LCQLSQGIYLTNRYMSISLVTAIAVD 113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STINSSVLPCPDYRPTHRILHLVVY-SLVLAAGLPIANALALWVFLRALRVHSVVSVXMCNL 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6 NTCGSSDLTWP---PAIKLGFYAYLGVLLVLGLLLNSLALWVFCCRMQQWTETRIYMTNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      42;
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33.7%; Pred. No. 4e-23;
tive 47; Mismatches 125; Indels
              PRIOR FILING DATE: 1999-03-12
PRIOR FILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: 60/136,436
PRIOR APPLICATION NUMBER: 60/136,436
PRIOR PILING DATE: 1999-05-28
PRIOR FILING DATE: 1999-05-28
PRIOR PILING DATE: 1999-05-28
PRIOR PILING DATE: 1999-05-28
PRIOR PELING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 60/136,557
PRIOR PELING DATE: 1999-05-28
PRIOR PILING DATE: 1999-05-28
PRIOR PILING DATE: 1999-05-28
PRIOR PILING DATE: 1999-05-29
PRIOR PELING DATE: 1999-06-29
PRIOR PELING DATE: 1999-06-29
PRIOR PELING DATE: 1999-06-29
PRIOR PILING DATE: 1999-09-29
PRIOR PILING DATE: 1999-00-17
PRIOR PILING DATE: 1999-00-17
PRIOR PILING DATE: 1999-10-01
                                                                                                                                                                                                                                                                                       A REFLICATION NUMBER: 60/137,127

R FILING DATE: 1999-05-28

R APPLICATION NUMBER: 60/137,131

R FILING DATE: 1999-05-28

R APPLICATION NUMBER: 60/141,448

R RILING DATE: 1999-06-29

R APPLICATION NUMBER: 60/156,653

R PILING DATE: 1999-09-29

R RILING DATE: 1999-09-29

R RILING DATE: 1999-09-29

R RILING DATE: 1999-09-29

R RILING DATE: 1999-09-29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    275 CYYYMAKEFQEA-SALAVAPRAK 296
APPLICATION NUMBER: 60/123,946
FILING DATE: 1999-03-12
APPLICATION NUMBER: 60/123,949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 60/157,282 PRIOR FILING DATE: 1999-10-01 NUMBER OF SEQ ID NOS: 74 SOFTWARE: Patentin Ver: 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 33.7%
Matches 109; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-875-076-4
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222 NLLVFVVCFLPLHVGLTVRLAVGWNA---CALLETIRRALYITSKLSDANCCLDAICYYY 278
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        176 TWKTYLSRIVIFIEIVGFFIPLILAVICSSMVLKTLTK--PVTLSRSKINKTKVLKMIFV 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  69 LLCTLPFVLHSLRDTSDTP----LCQLSQGIYLTNRYMSISLVTAIAVDRYVAVRHPLRA 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ------LLGFYLPLAVVVFCSLKVVTALAQRPPTDVGQAEATR-KAARMVWA 221
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 43;
                                                                                                                                                                                                                                                         TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein IIILE OF INVENTION: Coupled Receptor GPR2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 344;
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22.4%; Score 361.5; DB 1; Length
Best Local Similarity 29.2%; Pred. No. 4e-23;
Matches 90; Conservative 68; Mismatches 107; Indels
                                                                                                                                                                                                                                                                                                                                                       GOLDSTEIN & FOX P.L.L.C.
NW, SUITE 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
COMPATIEN: IBM PC COMPATIBLE
SYSTEM PC SYSTEM: PC-DOS/MS-DOS
SOFTMATIR RELEASE #1.0, VERSION #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 11488.1140003/EKS/KLM
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,948A
FILING DATE: 06-UN-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: PCT/US95/04079
FILING DATE: 30-MAR-1995
ATTORNEY/AGENT INFORMATION:
                                                                             APPLICANT: LI, YI
APPLICANT: CAO, LIANG
APPLICANT: NI, JIAN
APPLICANT: GENTZ, REINER
APPLICANT: STITCON III, GRANGER G.
APPLICANT: STITCON III, GRANGER G.
APPLICANT: ROSEN, CRAIG A.
Sequence 8, Application US/08467948A; Patent No. 5998164; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                               E: STERNE, KESSLER,
1100 NEW YORK AVE.,
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69 LLCTLPFVLHSLRDTSDTP----LCQLSQGIYLTNRYMSISLVTAIAVDRYVAVRHPLRA 124
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176 TWKTYLSRIVIFIEIVGPFIPLILMVTCSSMVLKTLTK--PVTLSRSKINKTKVLKMIFV 233
                                            222 NILVFVVCFLPLHVGLTVRLAVGWNA---CALLETIRRALYITSKLSDANCCLDAICYYY 278
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: SUTTON III, GRANGER G.
APPLICANT: SUTTON III, GRANGER G.
TITLE OF INVENTION: Polymucleotides Encoding Human G-Protein
TITLE OF INVENTION: Coupled Receptor GPR2
NUMBER OP SEQUENCES: 30
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1; Length 302;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.: 1100 NEW YORK AVE., NW, SUITE 600 WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
SOFTWARE: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,948A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04079
FILING DATE: 30-MAR-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22.3%; Score 360.5; DB 1; 30.0%; Pred. No. 4.3e-23; tive 64; Mismatches 103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: STEFFE, ERIC K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.1140003/EKS/KLM
TELECOMMUNICATION:
TELECHONE: 202-371-2600
TELEFRAX: 202-371-2540
                                                                                                                                                                                                                                                                                                                                                                                                                 GENTZ, REINER
BULT, CAROL J.
TII, GRANGER G.
                                                                                                                                                                                                                                                                                           Sequence 30, Application US/08467948A Patent No. 5998164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 30: SEQUENCE CHARACTERISTICS: LENGTH: 302 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 302 amino acids
TYPE: amino acid
STRANDEDNESS: abingle
TOPOLIGY: not relevant
MOLECULE TYPE: peptide
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CAO, LIANG
NI, JIAN
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                                                                                                                                    279 MAKEFQEA 286
                                                                                                                                                                           294 TSDTIQNS 301
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Best Local Similarity
Matches 90; Conserva
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APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66 FVPTLPFRIFYF-TTRNWPPGDLLCKISVMLFYTNWYGSILFLTCISVDRFLAIVYPFKS 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6 SSHCFYNDSFKYTLYGCMFSMVFVLGLISNCVAIXIFICVLKVRNETTTYMINLAMSDLL 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10 SSDLTWPPAIKLGFYAYL-GVLLVLGLLLNSLALWVFCCRMQOWTBTRIYMTNLAVADLC 68
                                                                                                                                                                                                                                                                                                           APPLICANT: GENTZ, REINER
APPLICANT: BULT, CAROL J.
APPLICANT: SUTTON III, GRANGER G.
APPLICANT: SUTTON III, GRANGER G.
APPLICANT: ROSEN, CRAIG A.
TITLE OF INVENTION: Coupled Receptor GPR1
CORRESPONDENCE: 30
CORRESPONDENCE: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREBT: 1100 NEW YORK AVE., NW, SUITE 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22.4%; Score 361.5; DB 2; Length 344; 29.2%; Pred. No. 4e-23; tive 68; Mismatches 107; Indels 43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVE., NW, SUITE 600
CITY: WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READBLE FORM:

AMDION TYPE: LOPPY DISK
COMPUTER: ELAPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,947A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04079
FILING DATE: 30-MAR-1995
ATTORNEY/AGENT INPORMATION:
NAME: STEEFE, ERIC K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: STEFFE, ERIC K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.1140002/EKS/KLM
TELECOMINICATION INFORMATION:
TELEPHONE: 202-371-2600
                                                                                                                                                                                                                          MAIL.
LI, YI
: CAO, LIANG
I: NI, JIAN
TT: GENTZ, REINER
TTI, CAROL J.
TII, GRANGER G.
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                                                                                                                                                                           // Sequence 8, Application US/08467947A
// Patent No. 6090575
// GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
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amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein
                  279 MAKEFQEA 286
                                                              294 TSDTIONS 301
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Best Local Similarity
Matches 90; Conserva
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                                                                                                                                 RESULT 11
US-08-467-947A-8
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APPLICANT: Liawitz, Kevin P.
APPLICANT: Liawitz, Kevin P.
APPLICANT: Behan, Dominic P.
APPLICANT: Behan, Dominic P.
APPLICANT: Chalmers, Derek T.
APPLICANT: Chalmers, Derek T.
APPLICANT: Lerner, Michael
TITLE OF INVENTION: Human G Protein-Coupled Receptors and Modulators Thereof
TITLE OF INVENTION: For the Treatment of Metabolic-Related Disorders
TITLE REFERENCE: 22.USG.CIP
CURRENT APPLICANTON NUMBER: US/10/314,048A
CURRENT FILING DATE: 2002-03-12
PRIOR FILING DATE: 2002-03-12
PRIOR FILING DATE: 2002-03-12
PRIOR PRILING DATE: 2002-07-29
PRIOR PILING DATE: 2002-07-29
PRIOR PILING DATE: 2002-07-29
PRIOR PILING DATE: 2002-08-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               143 LVIG----SLVARWILGIQEGGFCFR-STRHNF--NSMRFPLLGFYLPLAVVVFCSLKVV 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           196 TALAQRPPTDVGQAEATRKAARMVWANLLVFVVCFLPLHVGLTVRLAVGW-----NAC 248
                                                                                                                                                                                                                  170 STWKTYLSRIVIFIEIVGFFIPLILNVTCSTMVLRTL-NKPLTLSRNKLSKKVLKMIFV 228
                                                                                                                                                                                                                                                                                                     222 NLLVFVVCFLPLHVGL---TVRLAVGWNACALLETIRRALYITSKLSDANCCLDAICYYY 278
                                                                                                                                                                                                                                                                                                                                               ------LLGFYLPLAVVVFCSLKVVTALAQRPPTDVGQAEATRKAARMVWA 221
61 FVFTLPFRIYYF-VVRNWPPGDVLCKISVTLFYTNMYGSILFLTCISVDRFLAIVHPFRS 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            87 PL----COLSOGIYLTNRYMSISLVTAIAVDRYVAVRHPLRARGLRSPROAAAVCAVLWV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27 IGVLLVLGLLLNSLALWVFCCRMQQWTETRIYMTNLAVADLCLLCTLPFVLHSLRDTSDT
                                                         RGLRSPROAAAVCAVLWVLVI-GSLVARWLLGIQEGGFCFRST-RHNFNSMR-----FP-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 137, Application US/10314048A; Patent No. 6902902
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Connolly, Daniel
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Hakak, Yaron
Liaw, Chen
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Choi, Bryan
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         RGLRSPROAAAVCAVLWVLVI-GSLVARWLLGIQEGGFCFRST-RHNFNSMR-----FP- 176
                                                   170 STWKTYLSRIVIFIEIVGFFIPLILINVTCSTMVLRTL-NKPLTLSRNKLSKKKVLKMIFV 228
                                                                                                                                                                                                                                                         222 NLLVFVVCFLPLHVGL---TVRLAVGWNACALLETIRRALYITSKLSDANCCLDAICYYY 278
                                                                                                                                                                                                                                                                                            ------LLGFYLPLAVVVPCSLKVVTALAQRPPTDVGQAEATRKAARMVWA 221
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30.0%; Pred. No. 4.3e-23;
ive 64; Mismatches 103; Indels 43; Gaps
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APPLICANT: CAO, LIANG
APPLICANT: CAO, LIANG
APPLICANT: NI, JIAN
APPLICANT: NI, JIAN
APPLICANT: SUTTON LII, GRANGER G.
APPLICANT: NORMYNCES: 30
CORRESPONDENCE ADDRESS: 30
CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSES: ADDRESSES: ADDRESSES: ADSTREET: 1100 NEW YORK AVE., NW, SUITE 600
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COMPUTER: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.30
CURRENT APPLICATION NDATA:
APPLICATION NUMBER: US/08/467,947A
FILING DATE: 06-JUN-1995
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04079
FILING DATE: 30-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K.
REGISTATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.114000;
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-467-947A-30; Sequence 30, Application US/08467947A; Patent No. 6090575; GENERAL INFORMATION:
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INFORMATION FOR SEQ 1D NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 302 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
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Best Local Similarity 30.09
Matches 90; Conservative
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APPLICANT: Lerrant, Michael TILE OF INVENTION: Human G Protein-Coupled Receptors and Modulators Thereof TITLE OF INVENTION: Human G Protein-Coupled Receptors and Modulators Thereof FILE OF INVENTION: for the Treatment of Metabolic-Related Disorders FILE REFERENCE: 22.U56.CIP CURRENT APPLICATION NUMBER: U5/10/314,048A CURRENT FILING DATE: 2002-12-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      76 -VLHSLRD----TSDTPLCQLSQGIYLTNRYMSISLVTAIAVDRYVAVRHPLRARGLRSP 130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     39 RIDYYLRRRHWILGDIP-CRLVLFWLAMNRAGSIVFLTVVAVDRYFKVVFPHHMVNAISN 137
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: ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : || : ||| : ||| : ||| : ||| : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || 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33.2%; Pred. No. 2.1e-21;
tive 48; Mismatches 114; Indels 53; Gaps
                                                                                                                                                                                                           264 DIYSSVDLAFFTTLSFTYMNSMLDPVVYYFSSPSF 298
                                                                                                                                            249 ALLETIRRALYITSKLSDANCCLDAICYYYMAKEF 283
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PRIOR FILING DATE: 2002-03-12
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PRIOR PILING DATE: 2001-11-27
PRIOR PILING DATE: 2002-07-29
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PRIOR PILING DATE: 2002-08-19
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PRIOR PILING DATE: 2002-08-13
NUMBER OF SEQ ID NOS: 161
SOFTWARR: PALENTIN VETSION 3.1
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APPLICANT: Chen, Ruoping
APPLICANT: Stchman, Jeremy
APPLICANT: Comolly, Daniel
APPLICANT: Comolly, Daniel
APPLICANT: Leonard, James
APPLICANT: Leonard, James
APPLICANT: Hakak, Yaron
APPLICANT: Liaw, Chen
APPLICANT: Liaw, Chen
APPLICANT: Liaw, Chen
APPLICANT: Liaw, Chen
APPLICANT: Lowitz, Kevin P.
APPLICANT: Cominic P.
APPLICANT: Cerner, Michael
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Behan, Dominic P.
Chalmers, Derek T
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Antigenic peptides, such as for G protein-coupled receptors
(GPCRs), antibodies thereto, and systems for identifying such
antigenic peptides
Patent: WO 2061087-A 491 08-AUG-2002;
Lifespan Biosciences, Inc. (US)
Location/Qualifiers
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Sequence 491 from Patent
AX549206
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Homo sapiens CDNA FLJ23947 fis, clone HEP05863, highly similar to G protein coupled receptor GPR35.

AK172786
AK172786.

AK172786.1 GI:4707780
oligo capping; fis (full insert sequence).

Homo sapiens (human)
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Sugano, S. and Suzuki, Y.
Direct Submission

Direct Submission

Submitted (122-APR-2004) Sumio Sugano, Institute of Medical Science,
University of Tokyo, Laboratory of Genome Structure, Human Genome
Center; Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan
(E-mail:flcdna@mail.ims.u-tokyo.ac.jp, Tel:81-3-5449-5286,
Pax:81-3-5449-5416)
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Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini,
Hominidae, Homo.
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                                                                                                             TACCTGCCCCTGGCCGTGGTGGTCTTCTGCTCCCTGAAGGTGGTGACTGCCCTGGCCCAG
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/product=="G_protein-coupled_receptor"
/product=="G_protein-coupled_receptor"
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/db_xref="G1:2739109"
/db_xref="G1:2
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                                                                                  AF027957 1299 bp DNA linear PRI 17-FEB-1998
Homo sapiens G protein-coupled receptor (GPR35) gene, complete cds.
AF027957
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 (Dases 1 to 1299)
O'Dowd, B.F.
Direct Submission
Submitted (03-0CT-1997) Department of Pharmacology, University of Toronto, 8 Taddle Creek Rd., Toronto, ON MSS 1A8, Canada Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATGAATGGCACCTACAACACCTGTGGCTCCAGCGACCTCACCTGGCCCCCCAGCGATCAAG
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1 (bases 1 to 1299)

O'Dowd, B.F., Nguyen, T., Marchese, A., Cheng, R., Lynch, K.R., Heng, H.H., Kolakowski, L.F. Jr. and George, S.R.
Discovery of three novel G-protein-coupled receptor genes Genemics 47 (2), 310-313 (1998)
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/map="2q3.3"
214. .1143
/gene="GPR35"
/gene="GPR35"
/note="orphan G protein-coupled receptor"
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Pred. No. 9.6e-121;
0; Mismatches 3;
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al Similarity 99.7%;
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                                                        RESULT 3
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                            781 ACCAGCAAGCTCTCAGATGCCAACTGCTGGACGCCCATCTGCTACTACTACATGGCC
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Web site:http://genome.wustl.edu/gsc/index.shtml
Contact: submissions@watson.wustl.edu
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HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP
HOmo sapiens (human)
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                                                                                                                                                                                   901 CAGGACTCTGTGCGTGACCCTCGCCTAA 930
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3 (bases 1 to 169391)
Waterston, R.H.
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1 (bases 1 to 169391)
Waterston, R.H.
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NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan, cDNA full insert sequencing: Research Association for Biotechnology, cDNA library construction, 5' - & 3' - end one pass sequencing: Departent of Virology and Human Genome Center, Institute of Medical Science, University of Tokyo (partly supported by Science and Technology Agency).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 GCGCTCTGGGTGTTCTGCTGCCGCATGCAGCAGTGGACGGAGACCCGCATCTACATGACC 180
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                                                                                                                                                                                                                                                                                                 'note="cloning vector pME18SFL3"
                                                                                                                                                            /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="HEP05863"
                                                                                                                                                                                                                                    /cell line="HepG2"
/cell type="hepatoma"
/clone_lib="HEP"
                                                                                                                                                                                                                                                                                                                                                            99.14;
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AC111190
Homo saplens chromosome 2 clone RP13-511H14, WORKING DRAFT
SEQUENCE, 7 unordered pieces.
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Submitted (20-JUN-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
On Jun 14, 2002 this sequence version replaced gi:18699976.
                                                                 1783 AAGGAGTTCCAGGAGGCGTCTGCACTGGCCGTGGCTCCCCGTGCTAAGGCCCACAAAAGC 1842
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 (bases 1 to 169391)
Waterston, N.H.
Direct Submission
Submitted (18-FEB-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequencing vector: plasmid; 100$
Sequencing vector: plasmid; 100$
Chemistry: Dye-primer KT; 0$ of reads
Chemistry: Dye-terminator Big Dye; 100$ of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 167477 bases at least Q40
Consensus quality: 1681918 bases at least Q20
Consensus quality: 168194 bases at least Q20
Insert size: 185000; agarose-fp
Insert size: 185000; agarose-fp
Quality coverage: 9.60 in Q20 bases; sum-of-contigs
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us-10-083-168-84.rge

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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae; Homo.

Hominidae; Homo.

E 1 (bases 1 to 930)

Isolation of complete coding sequence for G-protein coupled receptor 35 (GPR35)

L Unpublished

E 2 (bases 1 to 930)

S Warren,C.N., Aronstam,R.S. and Sharma,S.V.

Direct Submission

L Submitted (11-ARR-2003) Guthrie cDNA Resource Center, Guthrie Complete to Submitted (11-ARR-2003) Guthrie Square, Sayre, PA 18840, USA

Research Institute, 1 Guthrie Square, Sayre, PA 18840, USA

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AY275467
Homo sapiens G-protein coupled receptor 35 (GPR35) gene, complete
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                                                                                                              TGGGTGCTGGTCATCGGCTCCCTGGTGGCTCGCTGGCGGATTCAGGAGGGCGGC
                                                                           TACATGAGCATCAGCCTGGTCACGGCCATCGCCGTGGACCGCTATGTGGCCGTGCGGCAC
                                                                                                                                                               CCGCTGCGTGCCCGGGGGTGCCCCCAGGCAGGCTGCGGCCGTGTGCGCGGTCCTC
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                     it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match

99.1%; Score 922; DB 14; Length 169391;
Best Local Similarity 99.5%; Pred. No. 8.8e-121;
Matches 925; Conservative 0; Mismatches 5; Indels 0;
                                                               581 5580: contig of 5580 bp in length 581 5680: gap of unknown length 194 17233: gap of unknown length 194 17233: gap of unknown length 195 17233: gap of unknown length 575 39574: gap of unknown length 675 64394: contig of 22281 bp in length 395 64394: contig of 24720 bp in length 675 64394: gap of unknown length 68227: contig of 18333 bp in length 6928 82277: gap of unknown length 6928 119522: contig of 36225 bp in length 6153 169391: contig of 50139 bp in length 6153 169391: contig of 50139 bp in length 6153 169391: contig of 50139 bp in length.
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119253. .169391
/note="assembly_name:Contig26"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /estimated length=unknown
82928. .119152
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119153. .119252
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/note="assembly_name:Contig23"
64395. .64494
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/note="assembly_name:Contig21"
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vector_side:right"
5581. .5680
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                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
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/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /chromosome="2"
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www.rzgu.de/garchingtoducts/microbingspicespinserinancessy www.rzgu.de/garchingtoducts/orfclones/
Contact: Inge Arlart
RZPD Deuterches Resourcenzentrum fuer Genomforschung GmbH,
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 101

www.rzgd.de
This clone is available from RZPD;
Contact RZPD (customer.serviceErzgd.de) for further information.
Clone ame at Harvard Institute of Proteomics
(www.hip.harvard.edu): FLH131000.01X
This CDS clone is part of a collection of human full ORF clones
jointly established and verified by the Harvard Institute of
Proteomics (HIP) and RZPD.
This CDS has been cloned incl. stopcodon.
The CDS has been inserted into pDONR201 via a BP Clonase(TM)
reaction. Additional sequence has been added in front of the start
codon: att. .AAAAAA GCA GCC TCC ACC (ATG).
The stopcodon is followed by the 3' att site: GACCCAGCTTCTT. att
The clone is validated by full sequence check.
Compared to the reference sequence NM_005301 (GI:33695096) we found
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CR541765 930 bp mRNA linear PRI 29-JUN-2004 Homo sapiens full open reading frame cDNA clone RZPDo834D0330D for gene GPR35, G protein-coupled receptor 35; complete cds, incl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   found
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www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=RZPDo834D0330D RZPDLIB;
Human Full ORF Clones Gateway(TM) - RZPD (kan-resist.) RZPD LIB No.
                                                                      780
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Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini,
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Genomforschung GmbH, Im Neuenheimer Feld 580, D-69120 Heidelberg,
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Halleck, A. Elsenstein, S.,
Neubert, P., Kstrang, K., Schatten, R., Shen, B., Henze, S., Mar, W.,
Korn, B., Zuo, D., Hu, Y. and LaBaer, J.
Cloning of human full open reading frames in Gateway (TM) system
entry vector (pDONR201)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 (Dases I to 930)
Halleck, A., Ebert, L., Mkoundinya, M., Schick, M., Eisenstein, S., Neubert, P., Kstrang, K., Schatten, R., Shen, B., Henze, S., Mar, W., Korn, B., Zuo, D., Hu, Y. and LaBaer, J.
Direct Submission
Submitted (28-JUN-2004) RZPD Deutsches Ressourcenzentrum fuer
                                                                                                                                                 781 ACCAGCAAGCTCTCAGATGCCAACTGCTGGAACGCCATCTGCTACTACTACTACTACATGGCC
                                                                                                                                                                                                                                                841 AAGGAGTTCCAGGAGGCGTCTGCACTGCCGTGGCTCCCAGTGCTAAGGCCCACAAAAGC
                                               721 CTCGCAGTGGGCTGGAACGCCTGTGCCCTCCTGGAGACGATCCGTCGCGCCCTGTACATA
                                                                                                                                                                                                                    AAGGAGTTCCAGGAGGCGTCTGCACTGGCCGTGGCTCCCCGTGCTAAGGCCCCACAAAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Full ORF shuttle clone, Gateway(TM), complete cds. Homo sapiens (human)
Homo sapiens
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DEFINITION
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VERSION
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SOURCE
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PCCRWQQWTETRIYWTNLAVADLCLLCTLPFVLHSLRDTSDTPLCQLSQGIYLTNRYM
SISLYTAIAVDRYYAYRHPLARRGLBSPRQAAAVCAVLWYLGSLVAGSIYARWLLGTQEGG
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VWANLLIYVVCVCPLPHYGLTVRLAVGRNACALLBTIRRALYTTSKLSDANCCLDAICY
YYMAKEFQEASALAVAPSAKAHKSQDSLCVTLA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6; Indels
                                                                                                                                                                                                             /gene="GPR35"
/codon start=1
/produc="G-protein coupled receptor 35"
/protein id="AAP3259 1"
/db_xref="G1:30526188"
                                                                                                                                                                /product="G-protein coupled receptor 35"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 920.4; DB 8;
Pred. No. 4.9e-120;
0; Mismatches 6;
organism="Homo sapiens"
                      l_type="genomic DNA"
_xref="taxon:9606"
                                                                                            gene="GPR35"
                                                                                                                                            gene="GPR35"
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Best Local Similarity 99.4%;
Matches 924; Conservative (
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/note="becnerichia coli DHSalpha T1 resistant"
from placenta and brain"
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sapiens clone FLH131000.01X G
35 (GPR35) mRNA, complete cds.
                                                                                                                  CTCGCAGTGGGCTGGAACGCCTGTGCCTCCTGGAGACGATCCGTCGCGCCCTGTACATA 780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cambridge, (04-JAN-12005) Biological Chemistry and Molecular Pharmacology, Harvard Institute of Proteomics, 320 Charles St., Cambridge, MA 02141, USA
This CDS clone is a part of a collection of human full-length rhis CDS clone is a part of a collection of human full-length rhis ORF clone has been cloned with normalized stop-codon. AttB recombination sites have been added to either end of the ORF and directionally cloned using the Gateway cloning system into pDONR 201. Additional sequences in the clone: 'ACC' before the 'ATG' (corresponding to ribosomal binding site and Kozak consensus sequences). Each clone is clonally isolated and full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           other sequences; artificial sequences.

1 (bases 1 to 930)
Halles, L., Taron, B., Jepson, D., Moreira, D., Raphael, J., Shen, B.,
Halleck, A., Koundinya, M., Hu, Y., Zuo, D. and LaBaer, J.
Cloning of human full-length CDS FLEXGene in
Gateway (TM) recombinational vector system
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hines, L., Taron, B., Jepson, D., Moreira, D., Raphael, J., Shen, B., Halleck, A., Koundinya, M., Hu, Y., Zuo, D. and LaBaer, J. Direct Submission
                               501 AGGCCACCCACCGACGTGGGGCAGGCAGGCCACCCGCAAGGCTGCCCGCATGGTCTGG
                                                                                                                                                                     ACCAGCAAGCTCTCAGATGCCAACTGCTGCTGGACGCCATCTGCTACTACATGGCC
                                                                                                                                                                                       841 AAGGAGTTCCAGGAGGCGTCTGCACTGGCCGTGCTCCCCGTGCTAAGGCCCAAAAGC
                                                                                                                                                                                                                                                          CTCGCAGTGGGCTGGAACGCCTGTGCCCTCGGAGACGATCCGTCGCCCCTGTACATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             organism="synthetic construct"
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/db_xref="taxon:32630"
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Human ORF Project.
synthetic construct
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/db_xref="G1:49456487"
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                                                                                                                                                       /clone_lib="Human Full ORF Clones Gateway(TM) - RZPD"
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 AA exchange(s) at position (first base of changed triplet): 880(ser-sarg)
Clone distribution: http://www.rzpd.de/products/orfclones/.
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                                                                                           /organism="Homo sapiens"
                                                                                                           /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="RZPDo834D0330D"
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Pred. No. 4.2e-120;
0; Mismatches 6;
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1 (bases 1 to 1875)
Horkawa,Y., Oda,N., Hanis,C.L., Bell Polymuclectides encoding calpain 10 Patent: US 6235481-A 21 22-MAY-2001;
Location/Qualifiers
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/organism="unknown"
/mol_type="unassigned
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PCCRMQQWTETRIYMTNLAVADLCLLCTLPFVLHSLRDTSDTPLCQLSQGIYLTNRYM
SISLYTA.TAVDRYVAVHPLARGLESPRQAANVCAVLWVIVGSLYNRWLLGTQBGG
PCFRSTRHNFNSMAFPLLGFYLDLAVVPCSLKVYTALAQRPPTDVGQARATKKAARM
VWANLLYPVVVCPLHHVGLTVRLAVGWNACALLETIRRALYITSKLSDANCCLDAICY
YYMAKEPQRASALAVAPRAKAHKSQDSLCVTLA"
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 xref="GI:60820956"
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
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    1875
    /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Ruarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
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    1236 GCCAACCTCCTGGTGTTCGTGGTCTGCTTCCTGCCCCTGCACGTGGGGCTGACAGTGCGC
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Pharmaceuticals AG (DE)
Location/Qualifiers
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1476 CAGACTCTCTGTGCGTGACCCTCGCCTAA 1505
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Mammalia, Eutheria, Euarchontoglires; Primates; Catarrhin;
Hominidae; Homo.

El (bases 1 to 1875)
Horikawa,Y., Oda,N., Cox,N.J., Li,X., Orho-Melander,M., Hara,M.,
Hinoklo,Y., Lindner,T.H., Mashima,H., Schwarz,P.E., del
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Bell,G.I.
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with type 2 diabetes mellitus
Inat. Genet. 26 (2), 163-175 (2000)
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Horikawa,Y. and Bell,G.I.
Direct Submitseion
Submitted (02-SEP-1998) Howard Hughes Medical Institute, The
University of Chicago, 5841 S. Maryland Avenue, MC1028, Chicago, IL
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Homo sapiens Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,

Homo sapiens (human)

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

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| OY 181 AACCTGGCGGTGGCCGACCTCTGCCTGTGCACCTTGCCCTTTCGTGCTGCTGCTGCTG 240   | Qy         241         CGAGACACCTCAGACACGCGGTGTGCCAGCTCTCCCAGGGGATCTACCTGACCAACGG 300           Db         43885         CGAGACACCTCAGACACCCGCTGTGCCAGCTCTCCCAGGGCATCTACCTGACCAACAGG 43944 | 0y 301 TACATGAGCATCAGCCTGGTCACGGCCATCGCCGTGCACCGCTATGTGGCCGTGCGGCAC 360<br>  | Oy         361         COGCTGCGTGCCCGCGGGCTGCCCCCAGGCAGGCTGCGGCCGTGTGCGCGGTCTC         420           Db         44005         CCGCTGCGTGCCGCGGGGCTGCGGTCCCCCAGGCAGGTGCGGCCGTGTGCGGGCTCTC         44064 | QY         421 TGGGTGCTGGTCATCGGTGGTGGTTGCTCGTGGGATTCAGGAGGCGGC 480           DD         44065 TGGGTGCTGGTCATCCTGCTGGTTGCTCGCTGGCTCCTGGGGATTCAGGAGGCGCC 41124        | Oy 481 ITCTGCTTCAGGAGCACCGGCACAATTTCAACTCCATGCGGTTCCGCTGCTGGGATTC 540 | OY 541 TACCTGCCCTGGCCGTGGTCGTTCTGCTCCCTGAAGGTGCTGCCCTGGCCCAG 600      | OY 601 AGGCCACCGACGGGGGGCAGGGCACCGCGAAGGCTAAACGCATGGTCTGG 660          | Qy 661 GCCAACCTCGTGTTCGTGTCTTCCTGCCCCTGCACGGGGCTGACAGTGCGC 720 | Qy         721 CTCGCRGGGCTGGAACGCCTGTGCCTCTGGAGACGATCCGTCGCGCCCTGTACATA 780           L                                      | 90                                       | Db 44485 Addadrrichdadagcgrcrccacraccccacracccacracccacaaagc 44544  Qy 901 Caggacrcrcrcrcrccccccccacaa 930  | RESULT 14 AF158748 LOCUS LOCUS DEFINITION Home sandens map 2037.3, genomic sequence. | AF158746<br>AF158748.3 GI:20260805<br>Homo sapiene (human)  | MISM   | REFERENCE 1 (bases 1 to 65674) AUTHORS Horkkawa,Y., Oda,N., Cox,N.J., Li,X., Orho-Melander,M., Hara,M., Hinokio,Y., Lindner,T.H., Mashima,H., Schwarz,P., del Bosque Plata,L., Horkawa,Y., Oda,Y., Yoshluchi, I., Colilla,S., | Polonsky, K.S., Wei, S., Concannon, P., Iwasaki, N., Schulze, J., Baier, L.J., Bogardus, C., Groop, L., Boerwinkle, E., Hanis, C.L. and Bell, G.I.  |
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| Qy         421 TGGGTGGTGATCGGCTCCCTGGTGGCTCGCTGGCTCCTGGGAATTCAGAAGGCCGC 480           Db         996 TGGTTGTTGATCATCGGTTGCTTGGTTGCTCCTGGGAATTCAGAAGGCGGC 1055 | Qy         481 TTCTGCTTCAGGAGCACCCGGCACAATTTCAACTCCATGCGGTTCCCGCTGCGGATTC 540           Db         1056 TTCTGCTTCAGGAGCACCCGGCACAATTTCAACTCCATGCGTTCCCGCTGCTGGGATTC 1115                   | OY         541 TACCTGCCCTGGCCGTGGTGTTTCTGCTCCCTGAAGGTGGTGACTGCCCTGGCCGG 600           Db         1116 TACCTGCCCTGGCCGTGGTGGTCTTCTGCTCCCTGAAGGTGGTGACTGCCCTGGCCCAG 1175 | Oy         601         AGGCCACCGACCGACGGGGGGGGGGGCCACCGGCAAGGCTAAACGCATGGTCTGG         660           Db         1176         AGGCCACCCACCGACGTGGGGCAGAGGCCACCCGCAAGGCTGCCCGCATGGTCTGG         1235     | Qy         661         GCCAACCTCCTGGTGTTCGTGGTCTGCTGCCCCTGCACAGGGGTTGACAGTGCGC         720           Db         1236         GCCAACCTCCTGGTGTTCGTGGTCTGCTTCCTGCCCTGC | QY 721 CTCGCAGTGGGCTGGAAACGCCTGTCGAGACGATCCGTCGCGCCCTGTACATA 780      | QY 781 ACCAGCAAGCTCTCAGATGCCAACTGCTGACGCCATCTGCTACTACTACTACTAGGCC 840 | Oy 941 AAGAAGTTCCAGAAGCGTCTGCACTGGCCGTGGCTCCCCGTGCTAAGGCCCACAAAAGC 900 | Oy 901 CAGACTCTCTGTGCGTGACCCTCGCCTAA 930                       | RESULT 13<br>AR153289<br>LOCUS AR153289 49136 bp DNA linear PAT 08-AUG-2001<br>DEFINITION Sequence 1 from patent US 6235481. | AR153289<br>AR153289.1 GI::1<br>Unknown. | ORGANISM Unknown. Unclassified.  NEFERENCE 1 (bases 1 to 49136)  AUTHORS Horikawa,Y., Oda,N., Hanis,C.L., Bell,G.I. and Cox,N.J.  TITLE Polynucleotides encoding calpain 10  TOURNAL Patent: US 6235481-AA 1 22-MAY-2001; | g.   | Query Match Best Local Similarity 99.0%; Score 920.4; DB 6; Length 49136; Best Local Similarity 99.4%; Pred. No. 2e-120; Matches 924; Conservative 0; Mismatches 6; Indels 0; Gaps 0; | OY 1 ATGAATGGCACCTACAACACCTGTGGCTCCAGCGACCTCACCCCAGCGATCAAG 60 | Oy 61 CTGGGCTTCTACGCCTACTTGGGCGTCCTGGTGCTAGGCCTGCTGCTGAAGCCTG 120   | Oy         121         GCGCTCTGGGTGTTCTGCTGCCGCATGCAGCAGCAGGAGACCCGCATCTACATGACC         180           Db         43.765         GCGCTCTGGGTGTTCTGCTGCCGCATGCAGCAGGAGACCCGCATCTCACATGACC         43.824 |

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| with type 2 diabetes mellitus  FURNED  11017071  REFERENCE 2 (base1 to 65674)  AUTHORS HORINAL Medical Institute, 5841 S. Maryland Avenue MC1028, Chicago, Howard Hughes JOURNAL Medical Institute, 5841 S. Maryland Avenue MC1028, Chicago, Illinois 60637, USA AUTHORS HORINAL Submitted (19-UAM-2001) The University of Chicago, Howard Hughes AUTHORS AUTHORS AUTHORS HORICAL Submission JOURNAL Sequence update by submitter REPRENCE 4 (bases 1 to 65674) AUTHORS HORINAL Submitted (12-ARR-2002) The University of Chicago, Howard Hughes AUTHORS HORICAL Submission JOURNAL Sequence update by submitter AUTHORS HORICAL Submission JOURNAL Sequence update by submitter REMARK Sequence update by submitter Location/Qualifiers  JOURNAL Submission JOURNAL Sequence update by submitter  AUTHORS JOURNAL Sequence update by submitter  JOURNAL SEAURINGS  JOURNAL SEAUR |                                    | variation 3269  variation /gene="RNPEPL1"  /replace="C" 34233563  /gene="RNPEPL1"  variation /gene="RNPEPL1"  /gene="RNPEPL1"  /gene="RNPEPL1"  /gene="RNPEPL1"  /note="UCSNP-128"  /replace="C"  /gene="RNPEPL1"  /note="UCSNP-129"  /replace="C"  /gene="RNPEPL1"  /note="UCSNP-131"  /gene="RNPEPL1"  /replace="C"  /replace=" |

| αγ             481             TTCTGCTTCAGGAGCACCAGGACTTTCAACTCCATGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG  | AC124862 N Homo sapienn AC124862 AC AC124862.4 HTG. Homo sapienn Homo sapienn Homo sapienn Homo sapienn Homo sapienn Hammalia; B Hominidas; Hominidas; Hominidas; Hominidas; Hominidas; Hominidas; Hominidas; Companion; Haakenson; Haakenson; The sequenc Upblistes; The bacquenc |  | AUTHORS Waterston, R.H.  TITLE Direct Submission JOURNAL Submission JOURNAL Submission JOURNAL Submission OURNAL School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA REFERENCE 5 (Dases 1 to 160111) AUTHORS Waterston, R.  TITLE Direct Submission JOURNAL Submitted (18-SEP-2002) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA REFERENCE 6 (bases 1 to 160111) |
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Direct Submission
Submitted (15-OCT-2002) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
7 (bases 1 to 160111)
71 (bases 1 but 180111)
71 (bases 1 but 180111)
72 (bases 1 but 180111)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mapping information for this clone was provided by Dr. Wes Warren, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Homo sapiens G protein-coupled receptor 35 (GPR35),
mRNA.; H NH0027M15.4
This gene was based on gi (4885320)"
                                                                                                                                                                                Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Prengen, B., Tateno, M., Catanses, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from and coworkers at http://www.chori.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          insert of the clone. This clone is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and respeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
                                                                                                                                                Submitted (15-APR-2005) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. MO 63108, USA.
On Sep 8, 2002 this sequence version replaced gi:22091410.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The sequence of AC080022 has been incorporated into AC124862 Location/Qualifiers
                                                                                                                                                                                                                                                                               Center: Washington University Genome Sequencing Center
Center code: WUGSC
                                                                                                                                                                                                                                                                                                                              NEIGHBORING SEQUENCE INFORMATION:
This sequence is not the entire inse
overlapped by AC011298 and AC110619.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="GPR35"
complement (4525. .5454)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement (4525. .5454)
                                                                                                                                                                                                                                                             Genome Center
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           http://genome.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="GPR35"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="GPR35"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MAPPING INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          restriction digest.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOURCE INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NOTICE:
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TITLE
                                                                                                    AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mRNA
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                                                                            REFERENCE
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This gene was based on gi(20070295)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GAAFTCLETARLDALHRQMIGLIGEDS PVSKLQVKLEPGVNPSHLAMLFTYEKGYCFV
YYLSQLCGDPQRFDDFLRAYVEKYKFTSVVAQDLLDSFLSFPPELKEQSVDCRAGLEF
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EPASEPSTELGKARADTDSDAQALLLGDEAPSSAISLRDVNVSA"
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38871. ,39139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement (join (36727. .36756,37010. .37055,37320. .37519,
38465. .38726,38886. .39088,40103. .40383,40698. .40864,
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48355. .48495)
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61516. .61632,62146. .62273))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(join(36303. 36756,37010. .37055,37320. .3751)
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41360. .41501,43257. .43474,44396. .44592,45933. .46064,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="CAPN10"

/note="Homo sapiens calpain 10 (CAPN10), transcript variant 1, mRNA; H NH0027M15.3
This gene was based on gi(13186301)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="CpG island (%GC=70.4, o/e=0.95, #CpGs=142)"
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                                                                                                                                                                                                                                                                    /note="CpG island (%GC=69.6, o/e=0.62, #CpGs=35)"
11914-.12354
fnote="CpG island (%GC=61.2, o/e=0.88, #CpGs=38)"
complement[16303..48672]
/gene="CAPN10"
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44479. .44861
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47989. .49201
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4915
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          541 TACCTGCCCTGGCCGTGGTGTTTCTGCTCCCTGAAGGTGGTGACTGCCCTGGCCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AACCTGGGGGGGGCCGACCTCTGCCTGTGCACCTTGCCCTTCGTGCTGCACCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CGAGACACCTCAGACACGCCGCTGTGCCAGCTCTCCCAGGGCATCTACCTGACCAACAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 ATGAATGGCACCTACAACACCTGTGGCTCCAGCGACCTCACCTGGCCCCCCAGCGATCAAG
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// note="CpG island (%GC=78.6, o/e=0.83, #CpGs=187)" (6197. 67466 |
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// note="CpG island (%GC=72.1, o/e=0.84, #CpGs=144)" (7157. 78247 |
// note="CpG island (%GC=72.1, o/e=0.84, #CpGs=105)" (7456. 1755985 |
// inner="CpG island (%GC=72.1, o/e=0.84, #CpGs=105)" (7456. 175588 |
// inner="CpG island (%GC=72.1, o/e=0.84, #CpGs=105)" (7456. 1155985 |
// inner="CpG island (%GC=72.1, o/e=0.84, #CpGs=105)" (7456. 1152985 |
// inner="CpG island (%GC=72.1, o/e=0.84, #CpGs=105)" (7456. 1152985 |
// inner="CpG island (%GC=72.1, o/e=0.84, #CpGs=105)" (7456. 1152588 |
// inner="CpG island (%GC=72.1, o/e=0.84, #CpGs=105)" (7456. 1152588 |
// inner="CpG island (%GC=72.1, o/e=0.84, #CpGs=105)" (7456. 1152588 |
// inner="CpG island (%GC=72.1, o/e=0.84, #CpGs=105)" (7456. 1152588 |
// inner="CpG island (%GC=72.1, o/e=0.84, #CpGs=105)" (7456. 1152588 |
// inner="CpG island (%GC=72.1, o/e=0.84, #CpGs=105)" (7456. 1152588 |
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99.0%; Score 920.4; DB 8; Length 160111;
Best Local Similarity 99.4%; Pred. No. 1.5e-120;
Matches 924; Conservative 0; Mismatches 6; Indels 0;
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Search completed: February 11, 2006, 04:54:32 Job time : 5119 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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- nucleic search, using sw model OM nucleic February 11, 2006, 00:25:50 Run on:

; Search time 684 Seconds (without alignments) 9061.643 Million cell updates/sec

US-10-083-168-84 930

Title: Perfect score:

1 atgaatggcacctacaacac......tgtgcgtgaccctcgcctaa 930 Sequence:

IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table:

4996997 seqs, 3332346308 residues Searched: 9993994 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 0B 0B Minimum | Maximum | Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

genesequ1990s:\* genesequ2001as:\* genesequ2001as:\* genesequ2002as:\* genesequ2002as:\* genesequ2003as:\* genesequ2003as:\* geneseqn1980s:\* N Geneseq 21:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. geneseqn2004as:\* geneseqn2004bs:\* geneseqn2005s:\*

geneseqn2003ds:\* geneseqn2003cs:\*

SUMMARIES

|        |       | ,     |                 |    | SOUTHWATES   | -                  |
|--------|-------|-------|-----------------|----|--------------|--------------------|
| Regult |       | Ouerv |                 |    |              |                    |
| No.    | Score | Match | Match Length DB | DB | ID           | Description        |
|        | 930   | 100.0 | 930             | 9  | ABS73401     | Abs73401 DNA encod |
| 8      | 925.2 | 99.5  | 930             | 9  | ABS73345     | Abs73345 cDNA enco |
| (1)    | 925.2 | 99.5  | 930             | 00 | ABZ42852     | Abz42852 Human G p |
| 4      | 925.2 | 99.5  | 930             | σ  | ADB67672     | Adb67672 Human G p |
| ហ      | 925.2 | 99.5  | 930             | 12 | AD029916     | Ado29916 Human GPC |
| •      | 925.2 | 99.5  | 930             | 14 | ADV73165     | Adv73165 Human col |
| 7      | 925.2 | 99.5  | 930             | 14 | AEB15038     | Aeb15038 cDNA enco |
| 60     | 922   | 99.1  | 1369            | ٣  | AAZ50891     | Aaz50891 Human rec |
| 6      | 920.4 | 99.0  | 1875            | m  | AAA27485     | Aaa27485 Human G p |
| 10     | 920.4 | 99.0  | 1875            | ۵  | ADA84068     | Ada84068 Human GPR |
| 11     | 920.4 | 99.0  | 1875            | 12 | AD078086     | Ado78086 Human GPR |
| 12     | 920.4 | 99.0  | 49136           | m  | AAA27475     | Aaa27475 NIDDM1 re |
| 13     | 919   | 98.8  | 1644            | 10 | ADF70563     | Adf70563 Orphan re |
| 14     | 917.2 | 98.6  | 3811            | 13 | ADR10415     | Adr10415 Full leng |
| 15     | 915.6 | 98.5  | 1043            | ٣  | AAZ35390     | Aaz35390 Human G-p |
| 16     | 900   | 96.8  | 1989            | 9  | ABZ35525     | Abz35525 Human gen |
| 17     | 838   | 90.1  | 858             | 12 | ADP28534     | Adp28534 Human sec |
| 18     | 549.2 | 59.1  | 924             | 12 | ADO3 0 2 0 6 | Ado30206 Mouse GPC |
| 19     | 514.2 | 55.3  | 599             | 13 | ADU11275     | Adul1275 Solid tum |
|        |       |       |                 |    |              |                    |

| Ac158361 Human col<br>Aad10133 Mouse G p<br>Ab135067 Murine cD<br>Adf87215 Single nu   | Aaa30740 DNA encod<br>Adc22744 Human G p<br>Adh14217 Mutated h<br>Aaa30581 Human G p<br>Aad26832 Human G p<br>Aac78113 Human G P | Adc2252 Human G P Adh13995 Human GPR Ado29766 Human nov Ab234905 Human gen | Aca58931 Farinesy,<br>Aca56831 Human sig<br>Adi56627 Human pol<br>Aad50858 Human G-P<br>Aba7741 Human G-P<br>Adf17570 Human G-P | Ado20684 Human GPR<br>Ads75991 Human GPR<br>Add71938 Human G-P<br>Ad171938 Human GPR<br>Ads19844 Human GPR<br>Adu06778 Human GPR |
|--|--|--|---|--|
| 14 ACL58361<br>4 AAD10133<br>6 ABL35067<br>10 ADF87215   | 3 AAA30740<br>10 ADC22744<br>10 ADH14217<br>3 AAA30581<br>6 AAD26832   | 10 ADC2522<br>10 ADH13995<br>12 ADC29766<br>6 ABZ34905                     | 10 ADES4834<br>10 ACAS6831<br>12 ADIS6627<br>8 AADS0858<br>12 ADE42741  | 12 ADO28684<br>13 ADS75991<br>6 AAD26831<br>12 ADL/1938<br>13 ADS1984<br>13 ADU06778   |
| 569<br>1854<br>1854  | 1098<br>1098<br>1089<br>1089   | 1089<br>1089<br>1365   | 1365<br>1365<br>1365<br>2693<br>2696  | 500<br>500<br>500<br>500<br>500<br>500<br>500<br>500<br>500<br>500   |
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## ALIGNMENTS

Human; transmembrane receptor; G-protein coupled receptor; GPCR; allergy; hypertension; reflux disease; depression; migraine; schizophrenia; ulcer; psychotic disorder; asthma; bronchospasm; anaesthesia; myocardial infarction; MI; stroke; glaucoma; anxiety; prostatic hyperplasia; epilepsy; prostate cancer; rhinitis; angina; prostatic hypertrophy; mutant; ds. DNA encoding human GPCR GPR35 mutant A216K. 멾 ABS73401 standard; DNA; 930 (first entry) 04-DEC-2002 ABS73401; RESULT 1 ABS73401 

WO200268600-A2. Homo sapiens. Synthetic.

06-SEP-2002.

26-FEB-2002; 2002WO-US005625.

26-FEB-2001; 2001US-0271913P.

(AREN-) ARENA PHARM INC.

Leonard JN; Maciejewski-Lenior D, Behan DP, Chalmers DT, Liaw CW, Charrier T. Ortuno D;

WPI; 2002-706980/76. P-PSDB; ABG95172.

New human G-protein coupled receptor (GPCR), useful for screening agonist or inverse agonist compounds for treating diseases associated with GPCR.

Example 2; Page 188-189; 201pp; English.

The present invention relates to transmembrane receptors, particularly

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(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (AREN-) ARENA PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chalmers DT,
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P-PSDB; ABG95159.
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endogenous human G-protein coupled receptors (GPCRs), mutant (non-endogenous) versions of the GPCRs, and the polynucleotide sequences encoding them. The GPCRs are useful for screening agonist or inverse agonist compounds for treating diseases associated with GPCR. Diseases that can be treated with such compounds include allergies, hypertension reflux disease, depression, migraine, schizophrenia, ulcers, psychotic disorders, asthma, bronchospasm, anaesthesia, myocardial infarction (MI), stroke, glaucoma, prostatic hyperplasia, epilepsy, prostate cancer, anxiety, prostatic hypertrophy, rhintis, and angina. The present
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The present invention relates to transmembrane receptors, particularly endogenous human G-protein coupled receptors (GPCRB), mutant (nonendogenous) versions of the GPCRs, and the polynucleotide sequences encoding them. The GPCRs are useful for screening agonist or inverse agonist compounds for treating diseases associated with GPCR. Diseases that can be treated with such compounds include allergies, hypertension, reflux disease, depression, magraine, schizophrenia, ulcers, psychotic disorders, asthma, bronchospasm, anaesthesia, myocardial infarction (MI), anxiety, prostatic hypertaplasia, epilepsy, prostate cencer, sequence encodes an endogenous human GPCR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; transmembrane receptor; G-protein coupled receptor; GPCR; allergy; hypertension; reflux disease; depression; migraine; schlzophrenia; ulcer; psychotic disorder; asthma; bronchospasm; anaesthesia; myocardial infarction; MI; stroke; glaucoma; anxiety; prostatic hyperplasia; epilepsy; prostate cancer; rhinitis; angina; prostatic hypertrophy; gene; ss.
                                 841 AAGGAGTCCAGGAGGCGTCTGCACTGGCCGTGGCTCCCCGTGCTAAGGCCCACAAAAGC 900
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inverse agonist compounds for treating diseases associated with GPCR.
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Pred. No. 1.9e-175;
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Best Local Similarity 99.7%;
Matches 927; Conservative
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The present invention describes antigenic peptides (I) comprising: (a) any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino caids. Also described: (I) an assay for the detection of a particular G protein-coupled receptor (GPCR) or a candidate polypeptide in a sample; and (2) an isolated antibody having high specificity and high affinity or cardial, the peridens of periods as GPCR modulators and in Gene therapy. The antigenic peptides for GPCRs are useful in detecting an autibody against a particular GPCR. (I) can be used as GPCR modulators and in Gene therapy. The peptides for GPCRs are useful in detecting an antibody against a particular GPCR, and in the production of specific antibody against a particular GPCR. The antigenic peptides for GPCRs and antibodies are useful for diagnosing and designing the presence of corresponding GPCRs. The antigenic peptides for GPCRs and antibodies are useful for diagnosing and designing drugs for treating immune-related diseases, growth-related disease, or autoimmune diseases, growth-related disease, or autoimmune diseases, e.g. AIDS, Alzheimer's disease, atherosclerosis, bacterial, fungal, protozoan or viral infections, osteoporosis, cancer, cardiamy chronic and acute inflammation, allergies, crohm's disease, diabetes, graft versus host disease, parkinson's disease, multiple sclerosis, path, psoriasis, cancer, cardiamy, pentiasis, cancer, cardiamy, pentiasis, cancer, cardiamy, pentiasis, con anxiety, depression, schizophrenia, dementia, mental retardation, memory loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension, cany other disorders, rheumatoid arthritis, trauma, ulcers, or any other disorder in which GPCRs are involved. The antibodies may be consisted in immunoassays and immunodiagnosis. ABCA2523 to ABZ42869 encode consistence of the proteins given in him and path of the proteins given in him to be a protein in which general in the penting of the proteins given in the penti
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human G protein-coupled receptor GPR35 nucleotide SEQ ID NO:491.
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ABZ42852
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Score 925.2; DB 8; Pred. No. 1.9e-175; 0; Mismatches 3;

99.5%;

927; Conservative

Similarity

Query Match est Local

Length 930;

Sequence 930 BP; 138 A; 328 C; 279 G; 185 T; 0 U; 0 Other;

exemplification of the present invention

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1 ATGAATGGCACCTACAACACCTGTGGCTCCAGCGACCTCACCTGGCCCCCAGCGATCAAG

ATGAATGGCACCTACAACACCTGTGGCTCCAGCGACCTCACCTGGCCCCCCAGCGATCAAG

121 GCGCTCTGGGTGTTCTGCTGCCGCATGCAGCGGACGGAGACCCGGCATCTACATGACC 180

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CTGGGCTTCTACGCCTACTTGGGCGTCCTGCTGGTGCTAGGCCTGCTGCTCAACAGCCTG

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New isolated antigenic peptides e.g., for G protein-coupled receptors (GPCR), useful for diagnosing and designing drugs for treating conditions in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or
                          osteoporosis, cardiomyopathy, inflammation; Crohn's disease; diabetes; graft versus host disease; Parkinson's disease; multiple sclerosis; pain; psoriasis; anxiety, depression; schizophrenia; dementia, memory loss; mental retardation; epilepsy; asthma; tuberculosis; obesity; nauses; hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma; ulcer; gene; ds.
Alzheimer's disease; atherosclerosis; infection; osteoarthritis;
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P-PSDB; ABP82002.
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The present invention relates to a method for predicting pathological conditions in heart failure using expression of one of 17 gene sequences (ADB67563-ADB67681); or protein sequences encoded by the genes (ADB67648-ADB67662). The proteins and genes are useful for diagnosis, treatment and prevention of heart failure.
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121 GCGCTCTGGGTGTTCTGCTGCCGCATGCAGGAGACGCGAACCCGCATCTACATGACC 180
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                                                                                                                                                                                                                                                     Predicting pathological conditions in heart failure using and proteins.
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                                                                                                                                                      Isomura T,
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99.7%; Pred. No. 1.9e-175;
tive 0; Mismatches 3;
                                                                                                                                                      Asakura M,
                                                                                                                                                                                                                                                                                                       Claim 1, Page 78; 137pp; Japanese.
                                      27-FEB-2003; 2003WO-JP002228.
                                                                     28-FBB-2002; 2002JP-00054388.
15-APR-2002; 2002JP-00112228.
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Best Local Similarity 99.7
Matches 927; Conservative
                                                                                                                                                    Kitakaze M, Takashima
Koishi R, Nakamaru K;
                                                                                                                     (SANY ) SANKYO CO LTD
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      04-SEP-2003
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claim 151; SEQ ID NO 1018; 542pp; English.

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Transgenic mouse; neurological disorder; adrenal gland disorder;

transgenic mouse; neurological disorder; adrenal gland disorder;

colon disorder; blood disorder; lamune disorder; bone disorder;

we muscular disorder; blood disorder; mutnitive disorder; cancer;

y idney disorder; netabolic disorder; nutritive disorder; cancer;

y wordy disorder; uterus disorder; prostate disorder; breast disorder;

kinhey disorder; uterus disorder; pancreas disorder; spleen disorder;

kynus disorder; thyroid disorder; pancreas disorder; spleen disorder;

thymus disorder; hyroid disorder; nutlarkinsonian; antimanic;

typuscatic; antiinflammatory; vasotropic; antidarhoteic; antidabetic;

virucide; hepatorropic; antibarcerial; antidarhoteic;

virucide; hepatorropic; antibarcerial; antidarhoteic;

wimmunosuppressive; nephrotropic; gene therapy; GPCR modulator; human;
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                                              GCCAACCTCTGGTGTTCGTGGTCTGCTTCCTGCCCTGCACGTGGGGCTGACAGTGCGC
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                                                                                                        CTCGCAGTGGGCTGGAACGCCTGTGGCCCTGGAGACGATCCGTCGCGCCCTGTACATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel mammalian G protein coupled receptors, useful for identifying compounds that modulates diagnosing and treating disease condition associated with GPCR dysfunction e.g. autoimmune diseases, angina
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Zeng H;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IE, Gragerov A, Hohmann J,
Pavlova MN, Vassilatis D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human GPCR GPR35 polynucleotide, SEQ ID NO:1018.
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Mcilwain KL, Pav
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P-PSDB; ADO29394.
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The invention relates to human and mouse G protein-coupled receptors (GPCRs) and nucleic acids encoding them. The invention also relates to sequences at least 90% identical to the GPCR proteins and nucleic acids of the invention; methods of treating, preventing or diagnosing diseases a sesociated with GPCRs of the invention; methods of screening for compounds useful in the treatment of GPCR-related diseases; a transgenic mouse comprising a GPCR pene of the invention; a mouse comprising a GPCR pene of the invention; a mouse comprising a GPCR pene of the invention; and kits comprising a GPCR pene of the invention; and kits comprising a GPCR pene of the invention; and kits comprising a GPCR pene of the invention; and kits comprising a GPCR pene of the invention; and kits comprising a GPCR nucleic acid. The GPCR nucleic acid. The GPCR nucleic acid and proteins may comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may comprise of the diagnosis, treatment or prevention of a wide variety of disorders of the advances. CC depression, diabetic neuropathy, Parkinson's disease or schizophrenia); disorders (e.g., Alzheimer's disease, disorders of the adrenal gland; disorders (e.g., Alzheimer's disease, compression; and disorders (e.g., angina, cardiac arrhythmia or syndrome); cardiovascular disorders (e.g., angina, cardiac arrhythmia or mycoardial infarction); muscular disorders (e.g., angina, cardiac arrhythmia or Albs); bone and joint disorders (e.g., angina, cardiac arrhythmia or Alberdamia or leukaemia); immune disorders (e.g., augina, cardiac arrhythmia or arthritis, gout or osteoporosis); metabolic or nutritive disorders (e.g., cancers). The pressent sequence argument disorders (e.g., cancers), the pressent sequence argument did not form part of the printed specification; rowardiac cardiac cardio of the invention. Note: The full sequence experient did not for
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99.5%; Score 925.2; DB 12;
Best Local Similarity 99.7%; Pred. No. 1.9e-175;
Matches 927; Conservative 0; Mismatches 3;
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                                  Sequence 930 BP; 138 A; 328 C; 279 G; 185 T; 0 U; 0 Other;
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                                                                  TACCTGCCCCTGGCCGTGGTGGTCTTCTGCTCCCTGAAGGTGGTGACTGCCCTGGCCCCAG
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A, Staten NR;
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Mazzarella RA,
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The invention relates to the use of human G-protein coupled receptor 35 (GPR35) for screening therapeutic agents useful in the treatment of cardiovascular disorders, liver and gastrointestinal diseases, cancer disorders, interactly diseases, metabolic diseases, hematological disorders, in a mammal. GPR35 is a G-protein coupled receptor (GPCR). The disorders, in a mammal. GPR35 is a G-protein coupled receptor (GPCR). The cherapeutic agents are screened by contacting a test compound with GPR35 cplypeptide, and detecting the binding of the test compound with GPR35 polypeptide. Also described are: (1) a method of diagnosing the above specified diseases in a mammal, comprising determining the amount of the GPR35 polymucleotide in healthy and/or diseased mammals comprising ctermining the amount of the GPR35 polymucleotide in healthy and/or diseased mammals (c) (2) a pharmaceutical composition for treating the above specified diseases in the mammal. comprising at that binds to the GPR35 polympetide; (3) use of regulators of a GPR35 for the preparation of the pharmaceutical composition, comprising identifying the comparation of the pharmaceutical composition, comprising identifying the comparation of the pharmaceutical carrier. GPR35 is useful for regulator with an acceptable pharmaceutical carrier. GPR35 is useful for compassion diseases, na mammal, and combining the correction testinal diseases, cancer disorders inflammatory diseases, concerning therapeutic agents for treating cardiovascular disorders, liver and gastrointestinal diseases, cancer disorders inflammatory diseases, neurological disorders and urological disorders repiratory diseases. This sequence encodes human GPR35.
                                                                                                                                                                                                              G-protein coupled receptor 35; GPR35; G-protein coupled receptor; GPCR; screening; cardiovascular disease; gastrointestinal disease; liver disease; cancer; neoplasm; metabolic disorder; hematological disease; respirator; respirator; cardiovascular-gen; neurological disease; urological disease; urological disease; arciovascular-gen; respiratory-gen; metabolic; antianemic; respiratory-gen; antiinflammatory; neuroprotective; uropathic; gene; se.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Screening of therapeutic agents useful in treating specified diseases involves contacting test compound with G-protein coupled receptor GPR35, and detect binding of test compound to polypeptide.
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                                           AEB15038 standard; cDNA; 930 BP.
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                           DB 14; Length 930;
C; 279 G; 185 T; 0 U; 0 Other;
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                        Score 925.2; DB 14
Pred. No. 1.9e-175;
0; Mismatches 3;
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                           99.5%;
    Sequence 930 BP; 138 A; 328
                                       Best_Local Similarity 99.7
Matches 927; Conservative
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                                                                                                                                                                                                                                      cytostatic; immunomodulatory; antiinflammatory; cardiant; antianaemic; antiarticosclerotic; hepacotropic; antiarthritic antirhemmatic; antiarthmatic; cardiantic; osteopathic; antiallergic; antidiabetic; dermatological; neuroprotective; diagnosis; treatment; prevention; reproductive disorder; cardiovascular; call proliferative; autoimmune; inflammatory; allergy; gastrointestinal; atherosclerosis; cirrhosis; leukaemia; cancer; AIDS; arthritis; anaemia; asthma; dermatitis; diabetes; osteoporosis; multiple sclerosis; irritable bowel syndrome; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New human receptor-associated proteins (HRAP) useful for the diagnosis, treatment and prevention of cell proliferative, autoimmune, inflammatory, reproductive, cardiovascular, and gastrointestinal disorders.
                                                                                                                                                                        Human receptor-associated protein cDNA from Incyte clone 3083742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Guegler KJ;
                                                                                                                                                                                                                     receptor-associated protein; HRAP; Incyte clone 3083742;
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99.1%; Score 922; DB 3; Length 1369;
Best Local Similarity 99.5%; Pred. No. 8.8e-175;
Matches 925; Conservative 0; Mismatches 5: Indela
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/*tag= a
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                        AAZ50891 standard; cDNA; 1369 BP
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Corley NC, Baughn MR;
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P-PSDB; AAY69989.
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ATGAATGGCACCTACAACACCTGTGGCTCCAGCGACCTCACCTGGCCCCCAGCGATCAAG 104

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                                 CCGCTGCCGCGCGCGCGCTCCCCCAGGCAGGCTGCGGCCGTGTGCGCGGTTCCTC
         AACCTGGCGGTGGCCGACCTCTGCTGCTGTGCACCTTGCCCTTGGGCTGCACTGCCTG
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non-insulin-dependent diabetes mellitus; CAPN10 gene; calpain 10;
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/transl_except= (pos:1095. .1097, aa:Arg)
/transl_except= (pos:1455. .1457, aa:Arg)
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Pred. No. 1.9e-174;
0; Mismatches 6;
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                                                                                      Location/Qualifiers
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Bell GI, Cox NJ;
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Local Similarity 99.4%;
les 924; Conservative
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(TEXA ) UNIV OF TEXAS SYSTEM.
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                                                          Homo sapiens
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Hanis CL, B
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Matches 924;
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ds; gene; tumour-associated antigen; TAg; cancer; lung cancer; breast cancer; prostate cancer; colon cancer; stomach cancer; pancreatic cancer; ear cancer; nose cancer; throat cancer; kidney cancer; cervical cancer; melanoma; tumour; human; GPR35.
936 CCGCTGCGTGCCCGCGGGCTGCGGTCCCCCAGGCAGGCTGCGGCCGTGTGTGCGCGGTCCTC 995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a novel method for determining if a nucleic acid is a marker for a predetermined phenotype/cell type of interest from a biological species. The method comprises performing a global comparatison of a group of expressed sequence tage (ESTS) known to be expressed in the phenotype/cell type of interest with all ESTS expressed in normal tissue in order to identify ESTS that are preferentially expressed in the phenotype/cell of interest. A method of the invention is useful for determining whether a nucleic acid is a marker for a predetermined phenotype or cell type of interest from a biological species, preferably Arabidopsis or human. The cell type of interest is an abnormal cell such as a tumour cell, and the predetermined phenotype is a stress-induced of the invention is also useful for determining the progression of colon cancer in a human, for detecting tumour cell, and for regulating or preventing the growth of a tumour cell. An antibody of the invention is useful for detecting the absence or presence of peptides encoded by tumour associated markers. A polypebide of the invention is useful as an animal. The present sequence encodes a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          240
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                                                                                                                                                                                                                                                                                                                                 Determining if a nucleic acid is a marker for a phenotype/cell type of interest, by global comparison of expressed sequence tags known to be expressed in the phenotype/cell type with all ESTs expressed in normal tissue.
                                                                                                                                                                                                                     Kozlov AP, Lobashev AV, Krukovskaya LL;
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99.0%; Score 920.4; DB 8; Length 1875;
Best Local Similarity 99.4%; Pred. No. 1.9e-174;
Matches 924; Conservative 0; Mismatches 6; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            immunogen for vaccinating an animal. The pr
tumour-associated antigen of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 23, Page 446-448; 516pp; English.
                                                             30-MAY-2001, 2001US-0293999P.
22-OCT-2001, 2001US-0330457P.
19-FEB-2002, 2002US-0357144P.
                    30-MAY-2002, 2002WO-IB004189
                                                                                                                                                                                                                   Baranova AV, Yankovsky NK,
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P-PSDB; ADA84069.
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1516. .3812
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                                       The invention relates to pharmaceutical compositions that comprise an agent that inhibits the expression or activity of a tumour-associated antigen (TAG) that is encoded by a nucleic acid. The pharmaceutical compositions and related compositions, are used for treatment of diseases associated with (abnormal) expression of TAG, specifically cancer e.g. of lung, breast, prostate, colon, stomach, pancreas, ear/nose/throat, kidney or cervix, also melanoma. Compositions containing TAG, or related nucleic acid, antibodies or host calls, are also useful for diagnosis and monitoring of tumours. The present sequence represents the human GPR35
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Pred. No. 1.9e-174;
0; Mismatches 6; Indels 0;
                                                                                                                                                Sequence 1875 BP; 290 A; 593 C; 614 G; 378 T; 0 U; 0 Other;
     compositions for diagnosis and monitoring.
                        Claim 1; SEQ ID NO 1; 124pp; German.
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Best Local Similarity 99.4%;
Matches 924; Conservative (
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                                                                                                                                                                                                                             Method for screening for type 2 diabetes mellitus comprises detecting polymorphism in a calpain encoding nucleic acid segment or a protease-encoding nucleic acid segment.
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                                                                                                                                                                                       WPI; 2000-339702/29.
P-PSDB; AaY79567, AaY79568, AaY79569, AaY79570, AaY79571, AaY79572,
AaY79573, AaY79574, AaY79576.
                                                                                                                                                              Otani K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99.0%; Score 920.4; DB 3; Length 49136; llarity 99.4%; Pred. No. 2.7e-174; Conservative 0; Mismatches 6; Indels 0;
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44922. .44927
                                                                                                                                                              Oda N, Sreenan S,
                                                                                                                                                                                                                                                                   Claim 65; Page 203-217; 257pp; English.
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(TEXA ) UNIV OF TEXAS SYSTEM.
                                                                                                      98US-0105052P.
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                                                                                                                                                             S, Horikawa Y, Oo
Bell GI, Cox NJ;
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Best Local Similarity
Matches 924; Conserva
                                              WO200023603-A2
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13-MAY-1999;
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Hanis CL, Be
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This invention relates to a novel method of identifying ligands to an orphan receptor protein which comprises transforming calls with DNA encoding a fusion protein of the orphan receptor with a fluorescent protein, so that the fusion protein is expressed in the cells (or cell membranes isolated from them) and contacting the cells with the potential ligand to be tested. A suitable fluorescent protein for incorporation in the fusion protein is green fluorescent protein (GPP), for example GFP-1, wild-type GFP, GFPPU or Bhlanced GFP (EGFP). The method is useful for the identification of ligands binding to an orphan receptor protein.
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                                                                                                                                                                                                                                                                    Komatsu H,
22-FEB-2002; 2002JP-00045728.
23-JUL-2002; 2002JP-00213949.
11-OCT-2002; 2002JP-00298237.
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Nagai K, Irie R;
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molecules are useful for diagnostic markers or therapeutic targets for the various diseases or morbid states. In particular, they are useful in gene therapy for treating osteoporosis, neurological disease, Alzheimer's disease, Parkinson's disease, dementia, short memory and various cancers, as well as for maintaining equilibrium of sense or motor function, and for treating emotional reaction, fear response and panic. Accordingly, they exhibit osteopathic, neuroprotective, nootropic, antiparkinsonian, cytostatic and tranquiliser activities. This polymucleotide is a full length human cDNA sequence of the invention. NoTS This sequence is not given in the sequence listing of the specification but can be obtained on CD-ROM from the European Patent Office, Vienna Sub-office.
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AAV58645), a novel member of the purinergic family of polypeptides and a
CG (*protein coupled receptor. The invention provides GPR35A polymcleotides
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                               3352 AAGGAGTTCCAGGAGGCGTCTGCACTGGCCGTGGCTCCCCGTGCTAAGGCCCACAAAAGC 3411
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               AAGGAGTTCCAGGAGGCGTCTGCACTGGCCGTGCTCCCCGTGCTAAGGCCCACAAAAGC
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                                                                                                                                                                                                                                                                 G-protein coupled receptor GPR35A cDNA.
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                                                                                                                                                                                                                                                1 ATGAATGGCACCTACAACACCTGTGGCTCCAGCGACCTCACCTGGCCCCCCAGCGATCAAG
                                                                                                                                                                   Gaps
                                                                                                                                                              ;
                                                                                 Length 1043;
C; 315 G; 206 T; 0 U; 0 Other;
                                                                                                                                                                   Indela
                                                                                     DB 3;
                                                                                                                                                                   6
                                                                                 Score 915.6; DB 3;
Pred. No. 1.6e-173;
0; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAGGACTCTCTGTGCGTGACCCTCGCCTAA 930
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    Sequence 1043 BP; 161 A; 361
                                                                                 / Match 98.5%;
Local Similarity 99.0%;
hes 921; Conservative
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Search completed: February 11, 2006, 09:42:57 Job time : 691 secs

This rage plank (usp.c.,

|                   |  | 23   | 374.4 | 40.3 | 701 | Ŋ | BY748928 |  |
|-------------------|--|------|-------|------|-----|---|----------|--|
|                   | GenCore version 5.1.7                              | C 24 | 338.4 | 36.4 | 372 | 7 | BF766676 |  |
|                   | Converight (c) 1993 - 2006 Biocceleration Ltd.     | c 25 | 335.4 | 36.1 | 736 | 7 | AI861901 |  |
|                   |  | c 26 | 317.6 | 34.2 | 444 | - | AW854188 |  |
|                   |  | C 27 | 317   | 34.1 | 429 | - | AW854178 |  |
| OM pincletc - pin | ON minjeto a minjeto aparch insting sw model       | 28   | 317   | 34.1 | 899 | ~ | BB629414 |  |
| or meters in      |  | 29   | 313.4 | 33.7 | 648 | 7 | CO957232 |  |
| Bun on .          | Pohram 11 2006 01:14:43 : Search time 4551 Seconds | 30   | 308   | 33.1 | 457 | - | AW854180 |  |
| wat out:          |  | 31   | 307.4 | 33.1 | 919 | N | BF151947 |  |
|                   | 9560 973 Million cell updates/sec                  | c 32 | 307   | 33.0 | 554 | N | BE696076 |  |
|                   |  | c 33 | 305.6 | 32.9 | 351 | - | AW854187 |  |
| E                 | 115-10-083-1-58-84                                 | C 34 | 300.8 | 32.3 | 448 | н | AW854198 |  |
| Dorfort goore.    | 0.00   | c 35 | 297.4 | 32.0 | 437 |   | AW854203 |  |
| Compace score:    | 1.0  | c 36 | 296   | 31.8 | 411 |   | AW854204 |  |
| · portentes       |  | c 37 | 296   | 31.8 | 571 | ~ | BE696051 |  |
| scoring rable.    | TIM WILL   | c 38 | 293.4 | 31.5 | 459 | - | AW854197 |  |
| SCOTTING CARTE:   | Control of Carpett 1 0                             | c 39 | 293.4 | 31.5 | 701 | 9 | CB321988 |  |
|                   |  | C 40 | 293   | 31.5 | 585 | Н | AW854051 |  |

82156650

41078325 seqs, 23393541228 residues

Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

| ALIGNMENTS  | AY401607 Homo sapiens GPR35 genomic survey seque AY401607 AY401607.1 GI:39757 GSS. Homo sapiens (human) Homo sapiens Bukaryota; Metazoa; |   | 2 (bases 1 to 930) Clark.A.G., Glanowski,S., Nielson,R., Thomarodd, M.A., Tanenbaum,D.M., Civello,D.R., Indexiera,S., Wang,G., Zheng,X.H., White,T., Adams, M.D. and Cargill,M. Adams, M.D. and Cargill,M. Submitted (16-NOV-2003) Celera Genomics, 4: Rockville, MD 20850, USA This sequence was made by sequencing genom them based on alignment. Location/Qualifiers ce 1.930 /organism="Homo sapiens"/mol_type="genomic DNA"/mol_type="genomic DNA"/mol_type="genomic DNA"/mol_type="genomic DNA"/mol_type="genomic DNA"/gene="GPR35"/locus_tag="HCM0947"  | Query Match 99.1%; Score 922; DB 10; Length 930;<br>Best Local Similarity 99.5%; Pred. No. 5.7e-191; Indels 0, Gaps<br>Matches 925; Conservative 0; Mismatches 5; Indels 0, Gaps |
|---|--|---|--|--|
| RESULT 1  | AY401607 LOCUS DEFINITION ACCESSION VERSTON KEYWORDS SOURCE ORGANISM   | REFERENCE AUTHORS TITLE JOURNAL PUBMED                                  | REFERENCE AUTHORS TITLE JOURNAL COMMENT FEATURES SOURCE GENE   | Query Match<br>Best Local<br>Matches 92  |
|   |  | ted by chance to have a of the result being printed, core distribution. | AY401607 Homo sapi CNB35420 AGENCOURT CNB35542 AGENCOURT CNB43697 AGENCOURT CO921702 AGENCOURT CO923163 AGENCOURT CO923163 AGENCOURT CO923163 AGENCOURT AY401609 Mus muscu AK036503 Mus muscu AK036503 Mus muscu CNB35586 AGENCOURT CO923285 AGENCOURT CO923285 AGENCOURT CNB32122 AGENCOURT   |  |
| Post-processing: Minimum Match 0%<br>Maximum Match 100%<br>Listing first 45 summaries | : EST:* 1: gb_est1:* 2: gb_est2:* 3: gb_est3:* 4: gb_htc:* 5: gb_est4:* 6: gb_est4:* 7: gb_est6:* 8: gb_est6:* 9: gb_est7:*              | > 0 +   | 99.1<br>79.2<br>79.2<br>65.6<br>64.6<br>63.6<br>63.6<br>61.4<br>759.1<br>63.6<br>778.7<br>63.6<br>778.7<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59.1<br>59. | 44.6 827 7<br>42.2 614 9<br>40.3 690 5   |
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Th., Wh. | 128 114 128 128 132 132 132 133 134 139 139 139 139 139 139 139 139 130 130 130 130 130 130 130 130 130 130 | DNA linea RANSCRIPT, par RANSCRIPT, par RE, Thomas, P., D.R., Lu,F., White, T.J., Sn m human-chimp- m, D.R., Lu,F., White, T.J., Sn m, tomas, P., Mnite, T.J., Sn | BY<br>BY<br>BY<br>BY<br>BY<br>BY<br>BY<br>BY<br>BY<br>BY | 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| _ | FEATURES<br>BOUR<br>Gene  | source<br>gene |  | 1. 6 d 1.     | 1930<br>/organism="Homo<br>/mol_type="geno"<br>/db_xref="taxon   |  | Home   | L. 930 /organism="Homo sapiens /mol_type="genomic DNA" /mol_type="genomic DNA" /db_xref="taxon:9606" /lo->930 | ens"<br>NA"  |   |   |  | •  |  |  |  |  |
|   | ORIGIN  | <b>!</b>       |  | /gene         | " m m  | ="GPR35<br>s_tag="   | .HG  | GPR35"<br>tag="HCM0947"   | _  |   |   |  |  |  |  |  |  |

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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
                      Homo sapiens (human)
Homo sapiens
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TITLE
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CEYWORDS
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CN834209 876 bp mRNA linear EST 02-JUN-2004 AGENCOURT 15864200 NIH MGC\_145 Homo sapiens cDNA clone 1MAGE:7001934 3', mRNA sequence.
CN834209.1 GI:47938609

RESULT 2 CN834209/c LOCUS DEFINITION

ACCESSION VERSION

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1..876
| organism="Homo sapiens"
| corganism="Homo sapiens"
| mol_type="mRNA"
| db_xref==taxon:9606"
| db_xref==taxon:9606"
| clone="IMAGE:7001334"
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| looe="wetor: pcDNA3.1" Site 1: varies by clone; Site 2: varies by clone; ORS were PCR-amplified and cloned into pcDNA3.1 by the GPCR Consortium. Cloning sites vary by clone and include the following: S' ESCORV-XMINI/KNot1.3', ScoRV (TA cloned, non-directional).
| For information about which gene each clones represents, please visit our anonymous ftp site at tp://image.llnl.gov/image.llnl.gov/image.llnl.gov/image.llnl.gov/image.llnl.gov/image.llnl.gov/image.llnl.gov/image.llnl.gov/image.llnl.gov/image.llnl.gov/image.llnl.gov/image.llnl.gov/image.llnl.gov/image.llnl.gov/image.llnl.gov/image.llnl.gov/image.llnl.gov/image.llnl.gov/image.llnl.gov/image.llnl.gov/image.llnl.gov/image.llnl.gov/image.llnl.gov/image.llnl.gov/image.llnl.gov/image.llnl.gov/image.llnl.gov/image.llnl.gov/image.llnl.gov/image.llnl.gov/image.llnl.gov/image.llnl.gov/image.llnl.gov/image.llnl.gov/image.llnl.gov/image.llnl.gov/image.llnl.gov/image.llnl.gov/image.llnl.gov/image.llnl.gov/image.llnl.gov/image.llnl.gov/image.llnl.gov/image.llnl.gov/image.llnl.gov/image.llnl.gov/image.llnl.gov/image.llnl.gov/image.llnl.gov/image.llnl.gov/image.llnl.gov/image.llnl.gov/image.llnl.gov/image.llnl.gov/image.llnl.gov/image.llnl.gov/image.llnl.gov/image.llnl.gov/image.llnl.gov/image.llnl.gov/image.llnl.gov/image.llnl.gov/image.llnl.gov/image.llnl.gov/image.llnl.gov/image.llnl.gov/image.llnl.gov/image.llnl.gov/image.llnl.gov/image.llnl.gov/image.llnl.gov/image.llnl.gov/image.llnl.gov/image.llnl.gov/image.llnl.gov/image.llnl.gov/image.llnl.gov/image.llnl.gov/image.llnl.gov/image.llnl.gov/image.llnl.gov/image.llnl.gov/image.llnl.gov/image.llnl.gov/image.llnl.gov/image.llnl.gov/image.llnl.gov/image.llnl.gov/image.llnl.gov/image.llnl.gov/image.llnl.gov/image.llnl.gov/image.llnl.gov/image.llnl.gov/image.llnl.gov/image.llnl.gov/image.llnl.gov/imag
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| Organism="Hono sapiens" |
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| Ab xref="reaxon:9606" |
| Clone="INAGE:7001933" |
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| Clone_lib="NIH_MGC_145" |
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/note="Vector: pcDNA3.1; Site 1: varies by clone; Site 2: varies by clone; ORFs were PCR-amplified and cloned into pcDNA3.1; by the GPCR Consortium. Cloning sites vary by clone and include the following: 5'-ECGRV-XmnI/KhoI-3', 5'-ECGRV-XmnI/KhoI-3', For information about which gene each clones represents, please visit our anonymous ftp site a constructional). ftp://image.lnn.gov/image/rearrayed_plates/IRBI.preSV.dat a Note: this is a NIH_MGC Library."
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varies by clone; ORFs were PCR-amplified and cloned into pcDNA3.1 by the GPCR Consortium. Cloning sites vary by clone and include the following: 5'-EcoRV-XmnI/NotI-3', EcoRV (TA cloned, non-directional).

for information about which gene each clones represents, please visit our anonymous ftp site at the fight//image/lnll.gov/image/rearrayed_plates/IRBI.preSV.dat a Note: this is a NIH_MGC Library."
                      EST 02-JUN-2004
                                                                                                                                                                                                                                  Hominidae, Homo.

E 1 (bases I to 960)

National Institutes of Health, Mammalian Gene Collection (MGC)

I Unpublished (1999)

National Institutes of Health, Mammalian Gene Collection (MGC)

I Unpublished (1999)

Contact: Daniela 8 Gerhard, Ph.D.

Office of Cancer Genomics

National Cancer Institute / NIH

Bldg. 31 Rml0A07 Bethesda, MD 20892

Email: cgapbe-remail.nih.gov

Tissue procurement: GPCR Consortium

CDNA Library Arrayed by: The I.M.A.G.E. Consortium

CDNA Library Preparation: GPCR Consortium

CDNA Library Preparation: GPCR Consortium

CDNA Library Preparation: GPCR Consortium

CDNA Library Arrayed by: The I.M.A.G.E. Consortium

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: IRBI3 row: a column: 02

High quality sequence stop: 568.

Location/Qualifiers
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                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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                  CN843697 960 bp mRNA linear EST
AGENCOURT 15864168 NIH_MGC 145 Homo sapiens cDNA clone
IMAGE:7001932 3', mRNA sequence.
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                                                                                                          CN843697.1 GI:47949352
                                                                                                                                                     Homo sapiens (human)
                                                                                                                                                                          Homo sapiens
                                                                                      CN843697
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                      LOCUS
DEFINITION
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 RmloAnd Bethesda, MD 20892
Email: cgapbs-remail.inh.gov
Tissue Procurement: GPCR Consortium
CDNA Library Preparation: GPCR Consortium
CDNA Library Arrayed by: The I.M.A.G.E. Consortium
CDNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MCC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
Plate: IRBIS row: d column: 11
High quality sequence stop: 407.
Location/Qualifiers
rce
                                                                           648 ACGCATGGTCTGGGCCAACCTCCTGGTGTTCGTGGTCTTCCTGCCCCTGCACGTGGG
                                                                                                                                          273 ccacardercradeccaaccrecregrerregrerregrerrecrececerecaeges
                                                                                                                                                                                                            708 GCTGACAGTGCGCCTCGCAGTGGGCTGGAACGCCTGTGCCCTCCTGGAGACGATCCGTCG
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1. (Dases 1 to 750)

NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (WGC)
Unpublished (1999)
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AGENCOURT 30698404 NIH_MGC_145 Homo sapiens cDNA clone IMAGE:7211833 3', mRNA sequence.
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Direct Submission Celera Genomics, 45 West Gude Drive, Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering them based on alignment.

Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                       Score 591.2; DB 10; Length 642; Pred. No. 1.1e-118;
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                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
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Science 302 (5652), 1960-1963 (2003) 14671302
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Best Local Similarity 93.3%;
Matches 599; Conservative
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a Note: this is a NIH_MGC Library."
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Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Buamalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Pan.
1 (bases 1 to 642)
Clark, A.C. Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
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                                                                            DB 7; Length 750;
                                                                                                             Indels
                                                                          Score 601.2; DB 7;
Pred. No. 7.5e-121;
0; Mismatches 19;
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AY401608.1 GI:39757597
                                                                              Query Match
Best Local Similarity 97.0%;
Matches 612; Conservative
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                                                                     301 TACATGAGCATCAGCCTGGTCACGGCCATCGCCGTGGACCGCTATGTGGCCGTGCGGCAC 360
                                                                                                                                                                                                                                                                                                                                                         421 TGGGTGCTGGTCATCGGCTCCCTGGTGGCTCGCTGGCTCCTGGGGATTCAGGAGGGCGGC 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  481 ITCTGCTTCAGGAGCACCCGGCACAATTTCAACTCCATGCGGTTCCCGCTGCTGGGATTC 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     541 TACCTGCCCTGGCCGTGGTGTCTTCTGCTCCCTGAAGGTGGTGACTGCCTGGCC 597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        513 TTCTGCTTCAGGAGCACCCGGCACAATTTCAACTCCATGGCGTTCCCGCTGGGGATTC
                                                                                                                                     1333 TACATGAGCATCAGCCTGGTCACGGCCATCGCCGTGGACCGCTATGTGGCCCTGCGGGCAC
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AGENCOURT 30842510 NIH_MGC_146 Homo sapiens cDNA clone
IMAGE37389770 3', mRNA sequence.
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/mol_type="mRNA"

/mol_type="mRNA"

/db_txef="texton:9606"

/clone="type="mixed"
/lab host="bling"

/lab host="bling"

/lab host="bling"

/lab host="bling"

/lab host="wector: pcDNA3.1; Site 1: varies by clone; Site 2:
varies by clone; ORF8 were PCR-amplified and cloned into
pcDNA3.1 by the GPCR Consortium. Cloning sites vary by
clone and include the following: 5'-EcoRV-XmnI/Khol-3',
5'-EcoRV-XmnI/NotI-3', EcoRV (TA cloned, non-directional).
For information about which gene each clones represents,
please visit our anonymous ftp site at
ftp://image.llnl.gov/image/rearrayed_plates/IRBI.preSV.dat
a Note: this is a NIH_MGC Library."
                   EST 16-AUG-2004
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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AGENCOURT 30488658 NIH MGC 145 Homo sapiens cDNA clone IMAGE:7211810 5', mRNA sequence.
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Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M. Birect Submission Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA Fockville, MD 20850, USA This sequence was made by sequencing genomic exons and ordering them based on alignment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 201 CIGCICCIIGCCAITIGIGCIGIACICCCCGGAAAIAIAGIICITCAGACACACCCGTCIG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 10; Length 924;
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Pred. No. 1.8e-109;
0; Mismatches 193;
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/organism="Mus musculus"
/mol type="genomic DNA"
/db_xref="taxon:10090"
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/locus_tag="HCM0947"
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Best Local Similarity 77.7%;
Matches 704; Conservative
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Mammalia; Butheria; Buarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
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1 Todd,M.A., Tanenbaum,D.M., Civello,D.R., Tu.F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
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Direct Submission

L. Submitted (16-7011-201) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN) Laboratory for Genome Exploration Research (RIKEN) Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 210-0045, Japan (E-mail:genome-resegec.riken.jp, Kanagawa 210-0045, Japan (E-mail:genome-resegec.riken.jp, Pax:81-45-503-9216)

Pax:81-45-503-9216)

Pax:81-45-503-9216)

CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Science Center and Genome Science Laboratory in RIKEN.
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Please visit our web site for further details.
URL:http://genome.gsc.riken.jp/.
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/db_xref="taxon:10090"
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/mol_type="mRNA"
/strain="C57BL/63"
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 2649)
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                                                                                                                   crecreccreareccarcratracracracareeccaeaagraccaegaagcerccae 860
                                                                                                                                                                                                               861 GCCAGCCAGTCTTCC---AACACACCCACAAGAGCCAAGATTCCCAGATCCTGAGCCT 917
      TGCTGCCCGAGACACCTTCAGCCGTGCCCTGTCCATCACAGGTAAACTCTCAGACACCAA 800
                                                             CTGCTGCCTGGACGCCATCTGCTACTACATGGCCAAGGAGTTCCAGGAGGCGTCTGC 863
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Mammalia, Butheria, Buarchontoglires, Glires, Rodentia,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AK036503 2649 bp mRNA linear HTC 03-APR-2
Mus musculus adult male bone CDNA, RIKEN full-length enriched
Library, clone:9830121M19 product:G protein-coupled receptor 35,
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                                                                                                                                                                             864 ACTGGCCGTGGCTCCCCGTGCTAAGGCCCACAAAAGCCAGGACTCTCTGTGCGTGACCCT
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HTC; CAP trapper.
Mus musculus (house mouse)
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Analysis of the mouse transcriptome based on functional annotation of Group Phase I k II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

Adachi, 7, Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Rodachi, J., Aizawa, K., Akimura, T., Hara, A., Hashizume, W., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Haranco, K., Miyazaki, H., Kawai, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Komno, H., Kouda, M., Kaya, S., Kurihara, C., Matuyama, T., Miyazaki, A., Murata, M., Nishi, K., Saitoh, H., Sakai, C., Sakai, K., Sakac, N., Sano, H., Sasaki, C., Sakai, K., Saito, R., Saltoh, T., Sakai, K., Shiraki, T., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sano, H., Sasaki, C., Sakai, K., Saitoh, M., Sakai, K., Shiraki, T., Sano, H., Shinasa, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatau, M. and Hayashizaki, Y. Takaku-Akahira, S., Submitseion Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Scholation Research Group, RIKEN Genomic Sciences Center (GSC), KRIKEN Yokohama Institute, 1-7-22 Suchiro-cho, Tsurumi-ku, Yokohama Institute, 1-7-22 Suchiro-cho, Tsurumi-ku, Yokohama Institute, 1-8-503-9222, URL: http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Chun. Muramaranda and Achamana Achamana Achamana and Achamana Ach
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pssqtrrnfsttafsilgfylplalvypcslqvytvlsrrpaadvgqaeatqkathmv
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(G (MGD|MGI:1929509, GB|NM_022320, evidence: BLASTN, 99%,
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/dev_gtage="12 days embryo"
Sumi, N., Ishli, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yananoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Yanamoto, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y., RIKRN integrated sequence analysis (RISA) system--384-format Genome Res. 10 (11), 1757-1771 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'tissue_type="embryonic body between diaphragm region and
                                                                                                                                                                                                                                                                                                                                               Exploration Research Group Phase II Team and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The FANTOM Consortium and the RIKEN Genome Exploration Research
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Please visit our web site for further details.
URL:http://fantom.gsc.riken.jp/
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Location/Qualifiers
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/db_xref="taxon:10090"
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/db_xref="GI:26330262"
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Mammalia; Butheria; Buarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus
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High-efficiency full-length cDNA cloning
weth. Enzymol. 303, 19-44 (1999)
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Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Pukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayachaida, K., Hayachan, T., Harozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katch, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Ohno, M., Ohazaki, Y., Saito, R., Saitoh, H., Sakai, K., Sakai, M., Taqami, M., Taqami, M., Taqawa, A., Takahashi, P., Takaku, Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y., Toya, T., Yasunishi, A., Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-langth cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
                                                                               HTC 03-APR-2004
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Yokohama,
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 4254)
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Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muridae, Murinae, Mus.
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4254 bp mRNA linear HTC 03-APR-Mus musculus NOD-derived CD11c +ve dendritic cells cDNA, RIKEN full-length enriched library, clone:F630036821 product:G
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                                                                                                                                                                                                                Gape
                                                                                                                                                                                                         6
                                                                                                                                            Length 3158;
                                                                                                                                                                                                         Indels
                                                                                                                                    Score 544.4; DB 4;
Pred. No. 2.2e-108;
0; Mismatches 196;
                                                                                                                                    sch 58.5%;
al Similarity 77.4%;
701; Conservative
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/clone lib="NIH MGC 145"
/note="Vector: pcDNA3.1; Site 1: varies by clone; Site 2:
/note="Vector: pcDNA3.1; Site 1: varies by clone; ORFS were PCR-amplified and cloned into pcDNA3.1 by the GPCR Consortium. Cloning sites vary by clone and include the following: 5'-EcoRV-XmnI/XhoI-3', 5'-EcoRV-XmnI/NotI-3', For information about which gene each clones represents, please visit our anonymous ftp site act plates/inage.lnll.gov/image/rearrayed_plates/IRBI.preSV.dat a Note: this is a NIH_MGC Library."
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                          1168 recrecceadacacerricaeccereccirercearecacadaraerercadacacea 1227
                                                                                                                                                                                                              1228 genecnecencianecanentariaciaentaciaecaagadagaginecaggaageeren 1287
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743
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1 (bases 1 to 783)

S NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Daniela S. Gerhard, Ph.D.

Coffice of Cancer Genomics

National Cancer Institute / NIH

BldG. 31 RmlOA07 Bethesda, MD 20892

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: GPCR Consortium

CDNA Library Preparation: GPCR Consortium

CDNA Library Preparation: GPCR Consortium

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

Plum through the I.M.A.G.E. Consortium/LLNL at:

Plum through the I.M.A.G.E. Consortium/LLNL at:

High quality sequence stop: 482.

High quality sequence stop: 482.
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
                                                                                   744 TGCCCTCCTGGAGGACGATCCGTCGCGCCCTGTACATAACCAGCAAGCTCTCAGATGCCAA
CTGCTTCCTGCCCCTGCACGTGGGGCTGACAGTGCGCCTCGCAGTGGGCTGGAACGCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CN835586 782 NIH_MGC_145 Homo sapiens cDNA clone IMAGE:7001933 5', mRNA sequence.
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db_xref="taxon:9666"

/clone="IMAGE:7001933"

/tissue_type="mixed"

/lab_host="DH10B"
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AUTHORS
TITLE
JOURNAL
COMMENT
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VERSION
KEYWORDS
SOURCE
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CN835586
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/cell type="NOD-derived CD11c +ve dendritic cells"
/clone lib="RIKEN full-length enriched mouse CDNA library"
428. .1352
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                          prepare mouse tissues.

Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Fissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust/MRC building Adenbrookes Hospital Cambridge) whose assistance we gratefully acknowledge.

Please visit our web site for further details.

URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/
Location/Qualifiers
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    Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                      /note="G_protein-coupled receptor 35 (MGD|MG1:1929509, GB|NM 022320, evidence: BLASIN, 99%, match=2495)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 4254;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 538.2; DB 4; Length 4
Pred. No. 5.2e-107;
0; Mismatches 193; Indels
                                                                                                                                                                                                                                                                                                               /db xref="FANTOM DB:F630036B21"
/db xref="taxon:10090"
                                                                                                                                                                                                                                           /organism="Mus musculus"
/mol_type="mRNA"
/strain="NOD"
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Best Local S
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Pred. No. 2.3e-102;
0; Mismatches 19;
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1 (bases 1 to 717)

S NIH-MGC http://mgc.nci.nih.gov/.

S NIH-MGC http://mgc.nci.nih.gov/.

L Upublished (1999)

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National Cancer Institute / NIH

Bldg. 31 RaloA07 Bethesda, MD 20892

Email: cgapbs-rømail.nih.gov

Tissue Procurement: GPCR Consortium

CDNA Library Preparation: GPCR Consortium

CDNA Library Preparation: GPCR Consortium

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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717 bp mRNA linear EST 16-AUG-2004 AGENCOURT 30698418 NIH_MGC_145 Homo sapiens cDNA clone
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                         Gaps
     Pred. No. 1.5e-105;
0; Mismatches 29; Indels
                         0; Mismatches
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        94.2%;
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| organism="Homo sapiens"
| organism="Homo sapiens"
| forganism="mkna"
| // white = "mkna" |
| // white = "wetor: pcDNA3.1; Site 1: varies by clone; Site 2: varies by clone; pcDNA3.1; Site 1: varies by clone; ORFS were PCR-amplified and cloned into yourse by clone and include the following: 5'-EcoRV-XmnI/Noc1-3', RcoRV (TA cloned, non-directional).
| for information about which gene each clones represents, please visit our anonymous ftp site at the first our anonymous ftp site at this is a NIH_MGC Library."
                                                                                                                                                                               Electronic memoral de la contrata; Eutebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homindae; Homo.

1 (Dases 1 to 1019)

1 (Dases 1 to 1019)

2 NIH-MGC http://mgc.nci.nih.gov/.

3 NIH-MGC http://mgc.nci.nih.gov/.

3 National Institutes of Health, Mammalian Gene Collection (MGC)

3 Unpublished (1999)

4 Contact: Daniela S. Gerhard, Ph.D.

5 Contact: Daniela S. Gerhard, Ph.D.

6 Cfice of Cancer Genomics

8 National Cancer Institute / NIH

8 Idg. 31 Rm.0A07 Bethesda, MD 20892

8 Email: cgapbs-rémail.nih.gov

7 Fissue Procurement: GPCR Consortium

CDNA Library Preparation GPCR Consortium

CDNA Library Arrayed by: The I.M.A.G.E. Consortium

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLML at:

http://image.llnl.gov

Plate: IRBI3 row: a column: 01

High quality sequence stop: 474.

High quality sequence stop: 474.
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CNB3Z1ZZ
AGENCOURT 15864152 NIH_MGC_145 Homo sapiens cDNA clone IMAGET7001931 3', mRNA sequence.
                                                                                                    CN832122.1 GI:47935875
                                                                                                                                            Homo sapiens (human)
Homo sapiens
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                                               719 GCCTCGCAGTGGGCTGGAACGCCTGTGCCCTCCTGGAGACGATCCGTCGCGCCCTGTACA
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| 9,                                 | Sequence 6, Appli<br>Sequence 6, Appli | Sequence 6, Appli | 9                                  | Sequence 3, Appli | 39                | 185,               | 240               | Sequence 18, Appl | Sequence 1391, Ap  | Sequence 1417, Ap  | 4                 | Sequence 171, App | 82                 | Sequence 74, Appl | Sequence 27, Appl | Sequence 1, Appli | Sequence 1, Appli |
|------------------------------------|--|-------------------|------------------------------------|-------------------|-------------------|--------------------|-------------------|-------------------|--------------------|--------------------|-------------------|-------------------|--------------------|-------------------|-------------------|-------------------|-------------------|
| US-08-599-654-6<br>US-08-485-573-6 | US-08-944-868A-6<br>US-08-944-423A-6   | US-08-925-743-6   | US-08-944-496-6<br>US-08-925-767-6 | US-09-875-076-3   | US-09-170-496D-39 | US-09-170-496D-185 | US-09-826-509-540 | US-08-405-271A-18 | US-09-016-434-1391 | US-09-023-655-1417 | US-10-087-345A-22 | US-09-976-594-171 | US-09-016-434-1482 | US-09-814-915A-74 | US-09-875-076-27  | US-08-442-134A-1  | US-08-444-581B-1  |
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| 87.8                               | 87.8<br>87.8                           | 87.8              | 87.8                               | 87.6              | 87.4              | 87.4               | 86                | 86                | 86                 | 98                 | 86                | 98                | 85.6               | 85.6              | 83.8              | 82.4              | 82.4              |
| 25<br>26                           | 27                                     | 53                | 30<br>31                           | 32                | 33                | 34                 | 35                | 36                | 37                 | 38                 | 39                | 40                | 41                 | 42                | 43                | 44                | 45                |

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ô 180 240 9 CTGGGCTTCTACGCCTACTTGGGCGTCCTGGTGCTAGGCCTGCTGCTCAACAGCCTG 181 AACCTGGGGGTGGCCGACCTCTGCCTGTGCACCTTGCCCTTCGTGCTGCACTCCTG 1 ATGAATGGCACCTACAACACCTGTGGCTCCAGCGACCTCACCTGGCCCCCAGCGATCAAG Gaps ô Sequence 21, Application US/09422869
; Batent No. 6235481
; GENERAL INFORMATION:
; APPLICANT: HOLINGWA, YUKIO
; APPLICANT: ODA, NAOHISA
; APPLICANT: CDA, NAOHISA
; APPLICANT: SKERNAN, SEAMUS
; APPLICANT: SKERNAN, SEAMUS
; APPLICANT: STREENAN, SEAMUS
; APPLICANT: STREENAN, SEAMUS
; APPLICANT: STREENAN, SEAMUS
; APPLICANT: HANIS, CRAIG I.
; APPLICANT: BENTUNION WETHODS OF TREATMENT OF TYPE 2 DIABETES
; TITLE OF INVENTION WINBER: US/09/422,869
; CURRENT FILING DATE: 1999-06-13
; EARLIER PILING DATE: 1999-06-13
; NUMBER OF SEQ ID NOS: 30
; SOOTWARE: Patentin Ver: 2.0
; SEQ ID NO 21
; LENGTH: 1875
; TVPE NAN Query Match
99.0%; Score 920.4; DB 3; Length 1875;
Best Local Similarity 99.4%; Pred. No. 2e-186;
Matches 924; Conservative 0; Mismatches 6; Indels 0; ORGANISM: Human US-09-422-869-21 61 ઠ 셤 δ ద ò 엄 8

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Query Match
Best Local Similarity 99.43
Matches 924; Conservative
               ; TYPE: DNA
; ORGANISM: Human
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                                    CGAGACACCTCAGACACGCCGCTGTGCCAGCTCTCCCAGGGCATCTACCTGACCAACAGG
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                                           Gaps
     Length 49136;
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                                         Indels
Score 920.4; DB 3;
Pred. No. 3.4e-186;
0; Mismatches 6;
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   99.0%;
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Behan, Dominic P.
APPLICANT: Chalmers, Derek T.
APPLICANT: Liaw, Chen W.
TITLE OF INVENTION: NO. 655339-Endogenous, Constitutively Activated Human G Protein-
TITLE OF INVENTION: Receptors
FILE REFERENCE: ARRN-0040
CURRENT APPLICATION NUMBER: US/09/170,496D
CURRENT APPLICATION NUMBER: 1998-10-13
NUMBER OF SEQ ID NOS: 294
SOPTWARE: Patentin version 3.1
SEQ ID NO 3
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87 CCTGCTGGTGCTAGGCCTGCTGCTCAACAGCCTGGGCGCTCTGGGTGTTCTGCTGCCGCAT
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Sequence 225, Application US/09170496D

Patent No. 6555339

GENERAL INFORMATION:
APPLICANT: Behan, Dominic P.
APPLICANT: Chalmers, Derek T.
APPLICANT: Liaw, Chen W.
TITLE OF INVENTION: No. 6555339-Endogenous, Constitutively Activated Human G Protein-TITLE OF INVENTION: Receptors
FILE REFERENCE: AREN-0040
CURRENT APPLICATION NUMBER: US/09/170,496D
CURRENT PILING DATE: 1998-10-13
NUMBER OF SEQ ID NOS: 294
SOFTWARE: PatentIn version 3.1
SEQ ID NO 225
LENGTH: 1098
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; Batent No. 6380362
; GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Watson, James D
; APPLICANT: Murison, James G
; TITLE OF INVENTION: Polynucleotides and methods for their use.
TITLE OF INVENTION: by the polynucleotides and methods for their use.
FILE REFERENCE: 11000.1050U1
; CURRENT FILING DATE: 1099-11-28
; FRIOR APPLICATION NUMBER: U.S. No. 6380362 60/171,678
; RIOR PILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSEQ for Windows Version 4.0
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Pred. No. 1.1e-14;
0; Mismatches 364;
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ilarity 50.4%;
Conservative (
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Matches 201; Conservative
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Best Local Similarity
Matches 403; Conserv
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; ORGANISM: Mouse
US-09-724-864-29
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; ORGANISM: Homo
US-09-170-496D-225
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US-09-170-496D-225
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US-09-724-864-29
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US-09-016-434-11429

i Sequence 1422) Application US/09016434

j Patent No. 650038

g GENERAL INFORMATION:
APPLICANT: Jafica Au-Young
APPLICANT: Jafica y J. Seilhamer

TITLE OF INVENTION: PATHWAY GENE EXPRESSION
TITLE OF INVENTION: PATHWAY GENE EXPRESSION
NUMBER OF SEQUENCES: 1490
CORRESPONDENCE ADDRESS:
ADDRESSES:
ADDRESSES:
ADDRESSES:
CONTY: PALO ALTO
STREET: 3174 PORTER DRIVE
COUNTRY: USA
ZIT: 94304

COUNTRY: USA
ZIP: 94304

MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                          12;
                                                                                                                                                                          Length 1089;
                                                                                                                                                                   Score 111.2; DB 3; Length 1 Pred. No. 1.4e-14; 0; Mismatches 293; Indels
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                            ; TYPE: DNA; ORGANISM: Homo sapiens
US-09-170-496D-3
                                                                                                                                                                   Query Match
Best Local Similarity
LENGTH: 1089
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,434
PILING DATE: HEREWITH
CLASSIFICATION OF PRIOR
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12.0%; Score 111.2; DB 3; 50.3%; Pred. No. 1.4e-14; ive 0; Mismatches 293;
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ATTORNEY/AGENT INFORMATION:
NAME: Zealer, Karen J.
REGISTRATION NUMBER: 37,071
REPERENCE/DOCKET NUMBER: 94-0002 US
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION FOR SEQ ID NO: 1429:
SEQUENCE CHARACTERISTICS:
LENGTH: 1365 base pairs
TYPE: nucleic acid
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Best Local Similarity 50.33
Matches 309, Conservative
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; CLONE: 9598152
US-09-016-434-1429
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                                                                                               Sequence 1, Application US/09850948
Patent No. 6919176
GENERAL INFORMATION:
APPLICANT: An, Songahu
APPLICANT: An, Songahu
APPLICANT: Thlarik Inc.
TITLE OF INVENTION: Polypeptides and Nucleic Acids Associated With Cancer FILE REPERENCE: 018/81-008300US
CURRENT APPLICATION NUMBER: US/09/850,948
CURRENT PILING DATE: 2001-05-07
NUMBER OF SEQ ID NOS: 2.1
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NAME/KEY: CDS
LOCATION: (594)..(1682)
OTHER INFORMATION: human G-protein coupled receptor 4 (GFR4)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 12.0%; Score 111.2; DB 3; Best Local Similarity 50.3%; Pred. No. 1.6e-14; Matches 309; Conservative 0; Mismatches 293;
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                                 905 rccccarccrcric 918
    GCTTCCTGCCCCTG
                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Homo sapiens
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LENGTH: 2693
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US-09-850-948-1
                                                                              RESULT 7
US-09-850-948-1
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Patent No. 6555339
GENERAL INFORMATION:
APPLICANT: Behan, Dominic P.
APPLICANT: Chalmers, Derek T.
APPLICANT: Liaw, Chen W.
TITLE OF INVENTION: No. 6555339-Endogenous, Constitutively Activated Human G I;
TITLE OF INVENTION: No. 6555339-Endogenous, Constitutively Activated Human G I;
TITLE OF INVENTION: No. 6555339-Endogenous, CONSTITUTION OF ENDOY.
TITLE OF INVENTION: 1998-10-13
TITLE OF INVENTION: 1998-10-13
TITLE OF INVENTION: 1998-10-13
TITLE OF INVENTION NUMBER: US/09/170,496D
CURRENT PELIG DATE: 1998-10-13
SOUTHWER OF SEQ ID NOS: 294
SOUTHWER OF SEQ ID NOS: 294
SEQ ID NO 117
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Best Local Similarity 50.2
Matches 402; Conservative
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US-09-170-496D-117
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690 GCTCAGCACCGTGGTCATCTTCCTGGCCTGCTTCCTGCCCTACCACGTGTTGCTGCTGGT 749
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                                                                                                                        510 cererecentrasecacralececareceareseasecececeareaeracraecraecra
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APPLICANT: Derk J. Bergsma, Catherine B. Ellis
TITLE OF INVENTION: A No. 5912335el G-Protein Coupled Receptor TITLE OF INVENTION: HUVCT36
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road, P.O. Box 1539
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406-0939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM 486
OPERATING SYSTEM: WINDOWS FOR WORKGROUPS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/724,974A
FILING DATE: October 3, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATG50022
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          837 GGCCAAGGAGTTCCAGGAGG 856
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REGISTRATION NUMBER: 34,344
REFERENCE/DOCKET NUMBER: ATC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610 270 5024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
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LENGTH: 1597
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STRANDEDNESS: Single
TOPOLOGY: Linear
NTI-SENSE: No
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; ANTI-SENSE:
US-08-724-974A-1
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GCTCAGCACCGTGGTCATCTTCCTGGCTTCCTGCCTTCCTGCTGCTGCTGCTTGTT 749
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                                                                                                                            GCGCCTCGCAGTGGGCTGGAACGCCTGTGCCCTCCTGGAGGACGATCCGTCGCGCCCTGTA 776
                                                                                                                                                                                                   CGTGCTGGTGGTGGCTTCCCCGGCCAACTGCCTGTCCCTCTACTTCGGCTACCTGCAGAT 149
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Patent No. 6319176

GENERAL INFORMATION

APPLICANT: Yang, Jianxin

APPLICANT: An, Songahu

APPLICANT: Tulaxif Inc.

APPLICANT: Songahu

APPLICANT: An, Songahu

APPLICANT: ON 18019001005

CURRENT PILING NUMBER: US/09/850,948

CURRENT FILING DATE: 2001-05-07

NUMBER OF SEQ ID NOS: 29

SSOTUARE: Patentin Ver. 2.1

ERNGTH: 1098
                                                                                                                                                                                                                                                                                           CATAACCAGCAAGCTCTCAGATGCCAACTGCTGCCTGGACGCCATCTGCTACTACAT
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50.2%; Pred. No. 2.4e-14;
tive 0; Mismatches 365; Indels 33; Gaps
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LOCATION: (1)..(1098)
OTHER INFORMATION: human G-protein coupled receptor 68 (GPR68, OGR1)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     837 GGCCAAGGAGTTCCAGGAGG 856
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Matches 402; Conservative
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US-09-850-948-5
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   Length 1597
Score 110; DB 2; Length 15
Pred. No. 2.6e-14;
0; Mismatches 365; Indels
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Patent No. 6653086
GENERAL INFORMATION:
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APPLICANT: Chalmers, Derek T.
APPLICANT: Liaw, Chen W.
APPLICANT: Lin, I-Lin
APPLICANT: Lowitz, Kevin P.
APPLICANT: Chen, Ruoping
   11.8%;
                  al Similarity 50.2
402; Conservative
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TITLE OF INVENTION: Endogenous, Constitutively Activated G Protein-Coupled Orphan Rece
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Pred. No. 2.6e-14;
0; Mismatches 365; Indels
                FILE REFERENCE: Aren0047
CURRENT APPLICATION NUMBER: US/09/364,425B
CURRENT FILING DATE: 2001-12-18
PRIOR APPLICATION NUMBER: 60/094,879
PRIOR FILING DATE: 1998-07-31
PRIOR FILING DATE: 1998-07-31
PRIOR FILING DATE: 1998-10-30
PRIOR FILING DATE: 1998-12-04
PRIOR APPLICATION NUMBER: 60/110,906
PRIOR APPLICATION NUMBER: 60/110,806
PRIOR PILING DATE: 1999-02-26
NUMBER: OF SEQ ID NOS: 60
SEQ ID NO 26
                                                                                                                                                                                                                                                                                                                       11.8%;
50.2%;
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Best Local Similarity 50.2
Matches 402; Conservative
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COCGANISM: Homo sapiens
US-09-364-425B-26
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Patent No. 6555339
GENERAL INFORMATION:
APPLICANT: Behan, Dominic P.
APPLICANT: Chalmers, Derek T.
APPLICANT: Liaw, Chen W.
TITLE OF INVENTION: Receptors
TITLE OF INVENTION: Receptors
FILE REFERENCE: AREN-0040
CURRENT APPLICATION NUMBER: US/09/170,496D
CURRENT APPLICATION NUMBER: US/09/170,496D
CURRENT FILING DATE: 1998-10-13
NUMBER OF SEQ ID NOS: 294
SOFTWARE: Patentin version 3.1
SEQ ID NO 193
LENGTH: 1128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Homo sapiens
US-09-170-496D-193
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                                                                                                                                                                                                                                                                                                        Sequence 165, Application US/09170496D
Patent No. 6555339
GENERAL INFORMATION:
APPLICANT: Behan, Dominic P.
APPLICANT: Liaw, Chen W.
TITLE OF INVENTION: No. 6555339-Endogenous, Constitutively Activated Human G Protein-TITLE OF INVENTION: No. 6555339-Endogenous, Constitutively Activated Human G Protein-TITLE OF INVENTION: No. 6555339-Endogenous, CONSTITLE OF INVENTION: No. 6555339-Endogenous, CONSTITLE OF INVENTION: No. 6555339-Endogenous, CONSTITLE OF SERVICATION NUMBER: US/09/170,496D
CURRENT APPLICATION NUMBER: US/09/170,496D
CURRENT FILING DATE: 1998-10-13
NUMBER OF SEQ ID NOS: 294
SOFTWARE: PatentIn version 3.1
FILE PROCESS OF THE OFFICE OFFICE OF THE OFFICE OF THE OFFICE OFF
1130 CTTCTCCCTCCTGCTCACCAGCTTCAACTGCGTGCCCGACCCCGTGCTTCTACTGCTTTCGT 1189
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11.8*; Score 109.6; DB 3; Length 1089;
Best Local Similarity 52.5*; Pred. No. 3e-14;
Matches 272; Conservative 0; Mismatches 234; Indels 12;
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US-09-170-496D-193
L', Seguence 193, Application US/09170496D
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ORGANISM: Homo sapiens
US-09-170-496D-165
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US-09-170-496D-165
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9.8%; Score 91; DB 3; Length 1815
Best Local Similarity 50.4%; Pred. No. 2.9e-10;
Matches 305; Conservative 0; Mismatches 290; Indels
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; Sequence 1, Application US/09041545
; Patent No. 6071719
; GENERAL INFORMATION:
    APPLICANT: HALSEY, WENDY S.
    APPLICANT: APPLICANT S.
    APPLICANT: HALSEY FORGE
    APPLICANT: HAPPLICANT S.
    APPLICANT S.

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OPERATING SYSTEM: DOS
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SOFTWARE: FESTEM: DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/041,545
FILING DATE: 11-MAR-1998
CLASSIFICATION DATA:
PRICR APPLICATION DATA:
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GRNERAL INFORMATION:
APPLICANT: Behan, Dominic P.
APPLICANT: Chalmers, Derek T.
APPLICANT: Liaw, Chen W.
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286 -TACCTGACCAACAGGTACATGAGCATCAGCCTGGTCACGGCCATCGCCGTGGACCGCTA 344
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Search completed: February 11, 2006, 06:07:54 Job time : 215 secs

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1: /cgn2_6/ptodata/1/pubpna/USO7_PUBCOMB.seq:*
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6: /cgn2_6/ptodata/1/pubpna/USIOB_PUBCOMB.seq:*
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Copyright (c) 1993 - 2006 Biocceleration Ltd.
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|           | Description              | Seguence 84, Appl | Sequence 15, Appl | Sequence 491, App  | Sequence 6, Appli | Sequence 21, Appl | Sequence 350, App | Sequence 1, Appli | Sequence 186, App | Sequence 17827, A   | Sequence 636, App | Sequence 1687, Ap  | Sequence 5959, Ap  | Sequence 61537, A   | Sequence 61547, A   | Sequence 61549, A   | _                   | Sequence 61552, A   | Sequence 61567, A   | Seguence 61568, A   | Seguence 61525, A   | Sequence 61532, A   | Sequence 61535, A   | Sequence 61565, A   |
| SUMMARIES | ΩI                       | US-10-083-168-84  | US-10-083-168-15  | US-10-225-567A-491 | US-10-696-639-6   | US-09-768-877-21  | US-10-157-031-350 | US-09-768-877-1   | US-10-505-486-186 | US-10-741-600-17827 | US-10-101-510-636 | US-11-060-756-1687 | US-11-060-756-5959 | US-10-741-600-61537 | US-10-741-600-61547 | US-10-741-600-61549 | US-10-741-600-61551 | US-10-741-600-61552 | US-10-741-600-61567 | US-10-741-600-61568 | US-10-741-600-61525 | US-10-741-600-61532 | US-10-741-600-61535 | US-10-741-600-61565 |
|           | Query<br>Match Length DB | 930 5             | 930 5             | 930 5              | 930 8             | 1875 3            | 1875 5            | 49136 3           | 1644 9            | 24477 8             | 1989 6            | 600 10             | 600 10             | 201 8               | 201 8               | 201 8               | 201 8               | 201 8               | 201 8               | 201 8               | 201 8               | 201 8               | 201 8               | 201 8               |
| de        | Query<br>Match Le        | 100.0             | 99.5              | 99.5               | 99.5              | 0.66              | 99.0              | 0.66              | 98.8              | 98.6                | 96.8              | 47.2               | 47.2               | 21.6                | 21.6                | 21.6                | 21.6                | 21.6                | 21.6                | 21.6                | 21.2                | 21.2                | 21.2                | 21.1                |
|           | Score                    | 930               | 925.2             | 925.2,             | 925.2             | 920.4             | 920.4             | 920.4             | 919               | 916.8               | 900               | 439.2              | 439.2              | 200.6               | 200.6               | 200.6               | 200.6               | 200.6               | 200.6               | 200.6               | 197.4               | 197.4               | 197.4               | 195.8               |
|           | Result<br>No.            | -                 | 8                 | e                  | 4                 | S                 | ø                 | 7                 | 80                | o                   | 10                | 11                 | 12                 | 13                  | 14                  | 15                  | 16                  | 17                  | 18                  | 19                  | 20                  | 21                  | 22                  | 23                  |

| Sequence 61546, A   | Sequence 61524, A   | Sequence 596, App  | Sequence 596, App | Sequence 225, App | Sequence 3, Appli | Sequence 1, Appli | Sequence 17, Appl | Sequence 1429, Ap  | Sequence 113, App  | Sequence 1, Appli | Sequence 1, Appli | Sequence 272, App  | Sequence 113, App | Sequence 456, App | Sequence 23834, A   | Sequence 2, Appli | Sequence 5, Appli | Sequence 147, App | Sequence 5, Appli | Sequence 117, App | Segmence 5, Appli |
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| US-10-741-600-61546 | US-10-741-600-61524 | US-09-866-050A-596 | US-10-152-661-596 | US-10-251-385-225 | US-10-251-385-3   | US-10-267-811-1   | US-10-101-510-17  | US-10-305-720-1429 | US-10-283-975A-113 | US-09-850-948-1   | US-10-273-575-1   | US-10-225-567A-272 | US-10-712-124-113 | US-10-101-510-456 | US-10-450-763-23834 | US-10-167-192-2   | US-10-400-991-5   | US-10-505-486-147 | US-09-850-948-5   | US-10-251-385-117 | 115-10-273-575-5  |
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| 201                 | 201                 | 1854               | 1854              | 1098              | 1089              | 1089              | 1365              | 1365               | 1365               | 2693              | 2693              | 2696               | 2696              | 2980              | 1149                | 1617              | 1617              | 1674              | 1098              | 1098              | 1098              |
| 18.6                | 16.2                | 15.2               | 15.2              | 12.0              | 12.0              | 12.0              | 12.0              | 12.0               | 12.0               | 12.0              | 12.0              | 12.0               | 12.0              | 12.0              | 11.9                | 11.9              | 11.9              | 11.9              | 11.8              | 11.8              | 11.8              |
| 1,72.6              | 150.6               | 141.8              | 141.8             | 111.6             | 111.2             | 111.2             | 111.2             | 111.2              | 111.2              | 111.2             | 111.2             | 111.2              | 111.2             | 111.2             | 110.4               | 110.4             | 110.4             | 110.4             | 110               | 110               | 110               |
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## ALIGNMENTS

| RESULT 1 US-10-083-168-84 Sequence 84, Application US/10083168 Publication No. US20030023069A1 GENERAL INFORMATION: APPLICANT: Liaw, Chen W. APPLICANT: Liaw, Chen W. APPLICANT: Haciolewski-Lenior, Dominique APPLICANT: Maciolewski-Lenior, Dominique APPLICANT: Leonard, James N. APPLICANT: Leonard, James N. APPLICANT: Lin, I-Lin ITILE OF INVENTION: Endogenous And No. US20; ITILE OF INVENTION: Receptors FILE REFERENCE: AREN-0320 CURRENT APPLICATION NUMBER: US/10/083,168 CURRENT APPLICANTON NO. US20030023069A1e1 S/US-10-083-168-84 | 200300230  |
|---|--|
| Query Match 100.0%; Score 930; Best Local Similarity 100.0%; Pred. No. 2 Matches 930; Conservative 0; Mismatch  | Score 930; DB 5; Length 930;<br>Pred. No. 2.6e-225;<br>Mismatches 0; Indels 0; Gaps 0; |
| Oy 1 ATGAATGGCACCTACAACACCTGTGGGTCCAC   | ATGAATGGCACCTACAACACCTGTGGCCTCCAGCGACCTCACCTGGCCCCCAGCGATCAAG 60                       |
|   |  |
| Oy 61 CTGGGCTTCTACGCCTACTTGGGCGTCCTGCT  | CTGGGCTTCTACGCCTACTTGGGCGTCCTGCTGGTGGTCTGCTGCTGCTCCAACACCTG 120                        |
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| Oy 121 GCGCTCTGGGTGTTCTGCTGCCGCATGCAGG  | GCGCTCTGGGTGTTCTGCTGCCGCATGCAGCAGTGGACGGAGCCCGCATCTACATGACC 180                        |
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| Oy 181 AACCTGGCGGTGGCCGACCTCTGCCTGTCTGTCTGTCTGT   | AACCTGGCGGTGGCCGCCTCTGCCTGCTGCACCTTCGCCCTTCGTGCTGCACCCCTG 240<br>                      |

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Sequence 6, Application US/10696639

Sequence 6, Application US/10696639

Publication No. US2005003743941

APPLICANT: Pharmacia Corporation

APPLICANT: Bourner, Mauren J.

TITLE OF INVENTION: DOLYPEPTIDES ENCODED THEREBY, AND METHODS OF USING THE FILE REPRENCE: 01040/1

FILE REPRENCE: 01040/1

CURRENT APPLICATION NUMBER: US/10/696,639

CURRENT FILING DATE: 2003-10-29

PRIOR APPLICATION NUMBER: 60/422,176

PRIOR PILING DATE: 2002-10-29

PRIOR PELING DATE: 2002-10-29

NUMBER OF SEQ ID NOS: 3114

SEQTIMARE: Patentin version 3.1

SEQ ID NO 6.
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                                  CTGGCAGTGGGCTGGAAGGCCTGTGCAGAGACGATCGCGCGCCCTGTACATA
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             CTCGCAGTGGGCTGGAACGCCTGTGGCCCTCCTGGAGACGATCCGTCGCGCCCTGTACATA
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Pred. No. 4.3e-224;
0; Mismatches 3;
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Best Local Similarity 99.7
Matches 927; Conservative
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CORGANISM: homo sapiens
US-10-696-639-6
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Sequence 491, Application US/10225567A

Publication No. US20030113798A1

GENERAL INFORMATION:
APPLICANT: LifeSpan Biosciences
APPLICANT: Brown, Joseph P.
APPLICANT: Brown, Joseph P.
APPLICANT: Burmer, Glenna C.
APPLICANT: Roush, Christine L.
TITLE POR INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
FILE REPERENCE: 1920-4-4
CURRENT FILING DATE: 2001-12-19
FRICA PAPLICATION NUMBER: 60/257,144
PRIOR FILING DATE: 2000-12-19
FRICA PROMARE: PALENTIN VERSION 3.1
SEQ ID NO 491
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SEQ ID NO 491
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Sequence 350, Application US/10157031
Publication No. US20030108890A1
GENERAL INFORMATION:
APPLICANT: Baranova, A. V.
APPLICANT: Karkovsky, N. K.
APPLICANT: Krakovskya, L. L.
TITLE OF INVENTION: In silico screening for phenotype-associated expressed sequences
FILE REPERENCE: 276-0103
CURRENT APPLICATION NUMBER: US/10/157,031
CURRENT FILING DATE: 2002-05-30
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APPLICANT: HORIKAMA, YUKIO
APPLICANT: ODA, NACHISA
APPLICANT: COX, NANCY J.
APPLICANT: COX, NANCY J.
APPLICANT: SREENAN, SEAMUS
APPLICANT: SREENAN, SEAMUS
APPLICANT: APPLICANT: KENICHI
APPLICANT: APPLICANT: MILL, GRAEME I.
TITLE OF INVENITON: METHODS OF TREATMENT OF TYPE 2 DIABETES
FILE REFERENCE: ARCIG: 307
CURRENT PILIGE DATE: 2001-01-23
FRIOR PILICATION NUMBER: 09/422,869
FRIOR FILING DATE: 1999-10-21
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PALENTIN VEY: 2.0
SOFTWARE: PALENTIN VEY: 2.0
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Pred. No. 7.1e-223;
0; Mismatches 6;
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Patent No. US20020150896A1
GENERAL INFORMATION:
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Matches 924; Conservative
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ORGANISM: Human
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US-09-768-877-21
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                                      RESULT 7

US-09-768-877-1

US-09-768-877-1

Sequence 1, Application US/09768877

Patent No. US20020150896A1

GENERAL INFORMATION:
APPLICANT: POLONSKY, KENNETH S.
APPLICANT: POLON, NAOHISA
APPLICANT: COX, NANCY J.
APPLICANT: COX, NANCY J.
APPLICANT: COX, NANCY J.
APPLICANT: COX, NANCY J.
APPLICANT: SREENAN, SEAWUS
APPLICANT: THOUS, CRAIG L.
APPLICANT: HANIS, CRAIG L.
APPLICANT: BELL, GRAEBE I.
TITLE OF INVENTION: WETHODS OF TREATMENT OF TYPI
CURRENT PLING DATE: 2001-01-23

PRIOR FILING DATE: 1999-10-21

NUMBER OF SEQ ID NOS: 30

SOFTWARKE: PATENTIN OF TYPI

LENGTH: 49136

TERGIT: APPLICATION NUMBER: 09/422,869

NUMBER OF SEQ ID NOS: 30

SEQ ID NO 1

LENGTH: 49136
1476 CAGGACTCTCTGTGCGTGACCCTCGCCTAA 1505
                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: DNA
; ORGANISM: Human
US-09-768-877-1
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                                                                                                         Length 1875;
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                                                                                                         99.0%; Score 920.4; DB 5; 99.4%; Pred. No. 7.1e-223; tive 0; Mismatches 6;
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                    3.1
      NUMBER OF SEQ ID NOS: 415
SOFTWARE: Patentin version
SEQ ID NO 350
LENGTH: 1875
                                                                                                                       Best Local Similarity 99.4 Matches 924; Conservative
                                                           tryPE: DNA
CORGANISM: Homo sapiens
US-10-157-031-350
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RESULT 9
US-10-741-600-17827
US-10-741-600-17827
Sequence 17827, Application US/10741600
Publication No. US20050026169A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
FILE REPRENCE: CL001499
CURRENT APPLICATION NUMBER: US/10/741,600
CURRENT APPLICATION NUMBER: US/10/741,600
CURRENT PILING DATE: 2003-12-22
NUMBER OF SEQ ID NOS: 73997
SEQ ID NO 17827
LENGTH: 24477
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Best Local Similarity 99.5%; Pred. No. 1.6e-222;
Matches 922; Conservative 0; Mismatches 5; Indels
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Squence 186, Application US/10505486

Publication No. US20050118639A1

GENERAL INFORMATION:

APPLICANT: Takeda Chemical Industries, Ltd.

TITLE OF INVENTION: Determination of a ligand
FILE REFERENCE: P03-0006FCT

CURRENT APPLICATION NUMBER: US/10/505,486

CURRENT APPLICATION NUMBER: J02-02-45728

PRIOR FILING DATE: 2002-02-22

PRIOR APPLICATION NUMBER: JP 2002-213949

PRIOR FILING DATE: 2002-07-23

PRIOR PLING DATE: 2002-07-23

PRIOR PLING DATE: 2002-07-23

PRIOR PLING DATE: 2002-07-23

PRIOR PLING DATE: 2002-07-23

PRIOR FILING DATE: 2002-07-10
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ORGANISM: Human
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Best Local Similarity 99.2%; Pred. No. 1e-217;
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PRIOR APPLICATION NUMBER: 60/276,947
PRIOR FILING DATE: 2001-03-20
NUMBER OF SEQ ID NOS: 805
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 636
LENGTH: 1989
TYPE: DNA
ORGANISM: Homo sapiens
PEATURE:
NAME/KEY: modified base
LOCATION: (1912)
OTHER INFORMATION: a, t, c, g, other of the control of the c
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Publication No. US20030148295A1
GENERAL INFORMATION:
APPLICANT: WANG, VIXIN
APPLICANT: WANG, VIXIN
TITLE OF INVENTION: EXPRESSION PROFILES AND METHODS OF USE
FILE REPERENCE: 15117.0012
CURRENT APPLICATION NUMBER: US/10/101,510
CURRENT FILING DATE: 2002-03-20
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US-10-101-510-636
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Sequence 5959, Application US/11060756
Publication No. US20050221354A1
GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Wyeth
APPLICANT: Wyeth
APPLICANT: Wounts, William Martin
APPLICANT: Wounts, William Martin
APPLICANT: Wounts, William Martin
APPLICANT: Wounts, Wolliam Martin
APPLICANT: Wounts, Wolliam Martin
APPLICANT: Wolliam Martin
APPLICANT: Wolliam Martin
APPLICANT: Target Genes
FILE REFERENCE: AM101083 (031896-042000)
CURRENT APLICATION NUMBER: US/11/060,756
CURRENT FILING DATE: 2005-02-18
NUMBER OF SEQ ID NOS: 303284
SOFTWARE: Patentin version 3.2
SEQ ID NO 5959
LENGTH: 600
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| Publication No. US20050026169A1
| GENERAL INFORMATION:
| GENERAL INFORMATION:
| GENERAL INFORMATION:
| TITLE OF INVENTION: GENERIC POLYMORPHISMS ASSOCIATED WITH
| TITLE OF INVENTION: WYCCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
| TITLE OF INVENTION: WYCCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
| TITLE OF INVENTION: WYCCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
| CURRENT APPLICATION NUMBER: US/10/741,600
| CURRENT PILING DATE: 2003-12-22
| NUMBER OF SEQ ID NOS: 73997
| SEQ ID NO 61537
| LENGTH: 201
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US-11-060-756-5959
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CORGANISM: Homo sapiens
US-10-741-600-61537
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US-10-741-600-61537
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TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
TITLE OF INVENTION: Target Genes
FILE REPERENCE: AM101083 (031895-042000)
CURRENT PAPPLICATION NUMBER: US/11/060,756
CURRENT FILING DATE: 2005-02-18
NUMBER OF SEQ ID NOS: 303284
SOFTWARE: Patentin version 3.2
SEQ ID NO 1687
                                                                                    994 TAACCAGCAAGCTCTCAGATGCCAACTGCTGGACGCCATCTGCTACTACTACATGG 1053
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                                                                                                                                                                                    CCAAGGAGTTCCAGGAGGCGTCTGCACTGGCCGTGGCTCCCCGTGCTAAGGCCCCACAAA
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47.2%; Score 439.2; DB 10;
Best Local Similarity 99.3%; Pred. No. 3.1e-101;
Matches 441; Conservative 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                          899 GCCAGGACTCTCTGTGCGTGACCCTCGCCTAA 930
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Publication No. US20050221354A1
REMAIL INFORMATION:
APPLICANT: Wyeth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Homo sapiens
US-11-060-756-1687
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Publication No. US20050026169A1

GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
FILLE REPRESENCE: CLOO1499

CURRENT APPLICATION NUMBER: US/10/741,600

CURRENT PILING DATE: 2003-12-22

NUMBER OF SEQ ID NOS: 73997

SEQ ID NO 61547

LENGTH: 201
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Publication No. US20050026169A1
GENERAL INFORMATION.
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: MYCCARDIAL INPARCTION, METHODS OF DETECTION AND USES THEREOF
FILE REPERENCE: CL001499
CURRENT APPLICATION NUMBER: US/10/741,600
CURRENT FILING DATE: 2003-12-22
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                                                                  223 TTCGTGCTGCACTCCCTGCGAGACACCTCAGACACGCCGCTGTGCCAGCTCTCCCAGGGC 282
                                                                                                                                       283 ATCTACCTGACCAACAGGTACATGAGCATCAGCCTGGTCACGGCCATCGCCGTGGACCGC 342
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 Score 200.6; DB 8; Length 201;
Pred. No. 6.4e-41;
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Query Match
Best Local Similarity 99.5%;
Matches 200; Conservative
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; ORGANISM: Homo sapiens
US-10-741-600-61547
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US-10-741-600-61549
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US-10-741-600-61547
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                                                                                                                                        Score 200.6; DB 8;
Pred. No. 6.4e-41;
1; Mismatches 0;
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, NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: PaetSEQ for Windows Version 4.0
; SEQ IN 00 61549
; LENGTH: 201
                                                                                                                                                                                                                                                                                                                                                                                                                                    GCTCCTGGGGATTCAGGAGGG 476
                                                                                                                                          Query Match 21.6%;
Best Local Similarity 99.5%;
Matches 200; Conservative
                                                                                       ; ORGANISM: Homo sapiens
US-10-741-600-61549
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Job time : 948 secs
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Sequence 30, Appl
Sequence 321, App
Sequence 61969, A
Sequence 61969, A
Sequence 36071, A
Sequence 36071, A
Sequence 36071, A
Sequence 36071, A
Sequence 3790, A
Sequence 3790, A
Sequence 3790, A
Sequence 2790, A
Sequence 2790, A
Sequence 28, Appl
Sequence 255, Appl
                                                                           February 11, 2006, 06:13:10; Search time 282 Seconds (without alignments) 2965.328 Million cell updates/sec
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1: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
2: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
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12: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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1 US-11-136-527-3805
US-10-750-185-32790
US-10-750-623-32790
1 US-11-136-527-3310
US-10-995-561-13208
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US-11-136-527-2954
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US-11-127-877-22
US-11-136-527-3778
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US-10-995-561-320
US-10-750-185-61969
US-10-750-623-61969
US-10-995-561-13298
US-10-750-185-36071
US-10-750-623-36071
                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
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| Sequence 463, App | Sequence 3314, Ap  | Sequence 3527, Ap  | Sequence 3005, Ap  | Sequence 8, Appli | Sequence 2101, Ap  | Sequence 2636, Ap  | Sequence 3673, Ap  | 'n                 | Sequence 608, App | Sequence 3421, Ap  | Sequence 7225, Ap  | Sequence 3129, Ap  | Sequence 1, Appli | Sequence 3742, Ap  | Sequence 9, Appli | Sequence 1, Appli | Sequence 2066, Ap  | Sequence 92, Appl | Sequence 684, App | Sequence 1, Appli | Seguence 466, App | Sequence 466, App | Sequence 3152, Ap  |
|-------------------|--------------------|--------------------|--------------------|-------------------|--------------------|--------------------|--------------------|--------------------|-------------------|--------------------|--------------------|--------------------|-------------------|--------------------|-------------------|-------------------|--------------------|-------------------|-------------------|-------------------|-------------------|-------------------|--------------------|
| US-11-136-527-463 | US-11-136-527-3314 | US-11-136-527-3527 | US-11-136-527-3005 | US-11-121-086-8   | US-11-136-527-2101 | US-11-136-527-2636 | US-11-136-527-3673 | US-11-136-527-3442 | US-11-136-527-608 | US-11-136-527-3421 | US-11-136-527-7225 | US-11-136-527-3129 | US-11-166-412-1   | US-11-136-527-3742 | US-10-533-355-9   | US-11-017-058-1   | US-11-136-527-2066 | US-11-122-329-92  | US-11-136-527-684 | US-10-513-118-1   | US-11-128-061-466 | US-11-128-049-466 | US-11-136-527-3152 |
| 11                | 11                 | 11                 | 11                 | 11                | 11                 | 11                 | 11                 | 11                 | 11                | 11                 | 11                 | 11                 | 11                | 11                 | 7                 | 11                | 11                 | 11                | 11                | ø                 | 11                | 1                 | 11                 |
| 1350              | 3129               | 2684               | 2693               | 246960            | 3635               | 1493               | 3883               | 4663               | 888               | 1524               | 1400               | 1769               | 2403              | 1560               | 1865              | 1876              | 1423               | 2215              | 8372              | 4357              | 2855              | 2855              | 1301               |
| 7.5               | 7.5                | 7.5                | 7.5                | 7.2               | 7.2                | 7.1                | 7.0                | 7.0                | 6.9               | 6.8                | 6.9                | 6.8                | 6.7               | 6.7                | 6.7               | 9.9               | 9.9                | 9.9               | 6.5               | 6.5               | 6.5               | 9.5               | 6.3                |
| 70.2              | 70.2               | 70                 | 70                 | 8.99              | 9.99               | 66.4               | 65                 | 65                 | 63.8              | 63.4               | 63.2               | 63.2               | 62.6              | 62.4               | 62.4              | 61.8              | 61.2               | 61                | 60.8              | 60.2              | 09                | 9                 | 59                 |
| 22                | 23                 | 24                 | 25                 | 26                | 27                 | 28                 | 29                 | 30                 | 31                | 32                 | 33                 | 34                 | 32                | 36                 | 37                | 38                | 38                 | 40                | 41                | 42                | 4.                | 44                | 45                 |

## ALIGNMENTS

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APPLICANT: Hoffmann, Marcel
APPLICANT: Hoffmann, Marcel
APPLICANT: Hoffmann, Marcel
APPLICANT: Hoffmann, Marcel
APPLICANT: Spittaels, Koenraad F. F.
APPLICANT: Spittaels, Koenraad F. F.
APPLICANT: Laenen, Wendy
TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
TITLE OF INVENTION: Amyloid-Beta Protein Production
FILE REFERENCE: P27,800-8 USA
CURRENT APPLICATION NUMBER: US/11/127,877
CURRENT FILING DATE: 2005-05-12
PRIOR FILING DATE: 2004-06-12
PRIOR FILING DATE: 2004-06-12
PRIOR FILING DATE: 2004-06-24
NUMBER OF SEQ ID NOS: 590
SOFTWARE: Patentin version 3.3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       207 GCTGTGCACCTTGCCCTTCGTGCTGCGAGACACCTCAGACACACGCCGCTGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 110; DB 11; Length 1523;
Pred. No. 3.7e-13;
0; Mismatches 365; Indels 33;
             Sequence 30, Application US/11127877 Publication No. US20050287565A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 11.8%;
Best Local Similarity 50.2%;
Matches 402; Conservative C
                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Homo sapiens US-11-127-877-30
                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 30
LENGTH: 1523
JS-11-127-877-30
                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
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Sequence 22, Appl Sequence 3778, Ap

Sequence

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APPLICANT: CARGILL, Michele et al.

TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF

TITLE OF INVENTION: DETECTION AND USES THEREOF

FILE REFERENCE: CLOO1559

CURRENT APPLICATION NUMBER: US/10/995,561

CURRENT FILING DATE: 2004-11-24

NUMBER OF SEQ ID NOS: 85702

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 320

LENGTH: 1498
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                                                                                                                                                                                                                                                                                      CGT-----GCTGCACTCCCTGCGAGAC---ACCTCAGACACGCCGCTGTGCCAGCTCTC 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             496
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257 GGTGGGCAACGCCCTGGTCATCTTCGTGATCCTTCGCTACGCAGGAGAAGACGCTAC 316
                                                                                                                                                               257 GGTGGGCAACGCCCTGGTCATCTTCGTGATCCTTCGCTACGCCAAGATGAAGACGGCTAC
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                                                                                         437 GCTCAGCGTCGACGCCTCAACATGTTCACCAGCGTCTTCTGTCTCTCACCGTGCTCAGCGT
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9.6%; Score 89; DB 7; Length 1498;
Best Local Similarity 55.5%; Pred. No. 5.1e-09;
Matches 217; Conservative 0; Mismatches 165; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGCTGCGGCCGTGTGCGCGGTCCTCTGGGTG 426
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     , ORGANISM: Homo sapiens
US-10-995-561-320
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; Sequence 61969, Application US/10750623
; Publication No. US20050287531A1
; GENERAL INPORMATION:
    APPLICANT: MAI GENOMICS, INC.
    APPLICANT: MAISE, Sue K.
    APPLICANT: RERR, Richard
    APPLICANT: RERR, Richard
    APPLICANT: ROSENFELD, David
    APPLICANT: RATH, Demnis
    APPLICANT: BATES, Stephen
    APPLICANT: PANTIN, Demnis
    APPLICANT: PANTIN, Demnis
    TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
    TITLE OF INVENTION: METHOD ADDE: 2003-12-31
    PRIOR PILING DATE: 2003-12-31
    PRIOR PILING DATE: 2002-12-31
    NUMBER OF SEQ ID NOS: 64922
    SOFTWARE: PATENTIN Version 3.1
    SOFTWARE: PATENTIN Version 3.1
    SUMMER OF SEQ ID NOS: 64922
    SOFTWARE: PATENTIN VERSION 3.1
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Pred. No. 5.3e-09;
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US-10-750-623-61969
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                                                                                                                                                                    Sequence 61969, Application US/10750185
; Sequence 61969, Application US/10750185
; Publication No. US2005026603A1
; GENERAL INFORMATION:
; APPLICANT: WI GENOMICS, INC.
; APPLICANT: RERR, Richard
; APPLICANT: ROSENFELD, David
APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TILLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; TILLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; TILLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: WM11100-2
; CURRENT APPLICATION NUMBER: US 60/437,482
; FRIOR APPLICATION NUMBER: US 60/437,482
; RIOR APPLICATION NUMBER: US 60/437,482
; RIOR APPLICATION NUMBER: US 60/437,482
; SOFTWARE: PATENTIN VERSION 3.1
; SEQ ID NOS: 64922
; SOFTWARE: PATENTIN VERSION 3.1
; LENGTH: 2095
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Pred. No. 5.3e-09;
0; Mismatches 410; Indels
                  557 GGCCAAGCTCATCAACCTGGGCGTGTGGCTG 587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: DNA
; ORGANISM: Bovine 19866880917942
US-10-750-185-61969
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al Similarity 47.9%;
402; Conservative
                                                                                                                                                                 US-10-750-185-61969
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Best Local S:
Matches 402
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6438 GCTCAGCGTCGACGGCCTCAACATGTTCACCAGCGTCTTCTGTCTCACCGTGCTCAGCGT 6497
                                                                                                                                      1333 CATCTCTTCATCTACTCCGTGGTGTGCCTGGTGGGGCTCTGTGGGAACTCCATGGTCAT 1274
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                                                                                    336 GGACCGCTATGTGGCCGTGCGGCACCCGCTGCGTGCCCGCGGGCTGCGGTCCCCCCAGGCA 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   297 CAGGTACATGAGCATCAGCCTGGTCACGGCCATCGCCGTGGACCGCTATGTGGCCGTGCG 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cenengagnacia de transporte de la constanta del constanta de la constanta de l
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  357 gCACCCGCTGCGTGCCCGCGGGTGCGGTCCCCCCAGGCTGCGGCCGTGTGCGCGGT
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6
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APPLICANT: DATE CENOMICS, INC.

APPLICANT: CERR, Richard

APPLICANT: RERR, Richard

APPLICANT: ROSENFELD, David

APPLICANT: HOLM, Tom

APPLICANT: APPLICANT: BATES, Stephen

APPLICANT: PANTIN Demnis

TITLE OF INVENTION: COMPOSITIONS FOR INPERRING BOVINE TRAITS

TITLE OF INVENTION: COMPOSITIONS FOR INPERRING BOVINE TRAITS

CURRENT APPLICATION NUMBER: US/10/750,185

CURRENT FILING DATE: 2003-12-31

PRIOR PILING DATE: 2002-12-31

NUMBER OF SEQ ID NOS: 64922

SOFTWARE: PALCATION VETSION 3.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 88.2; DB 7;
Pred. No. 7.4e-09;
                                                                                                                                                                                                                                                                                                                           5558 GGCCAAGCTCATCAACCTGGGCGTGTGGCTG 6588
                                                                                                                                                                                                                                               396 GGCTGCGGCGTGTGCGCGGTCCTCTGGGTG 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 36071, Application US/10750185
Publication No. US20050260603A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Bovine 19866880675545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 49.3%;
Matches 265; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 7
US-10-750-185-36071/C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-750-185-36071
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 1685
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Publication No. US20050272054A1

GRNERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GRNETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REFERENCE: CLO1559
CURRENT PILICHING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12288
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593
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APPLICANT: MAI GENOMICS, INC.
APPLICANT: MAI GENOMICS, INC.
APPLICANT: David
APPLICANT: MAILHOO-1
CURRENT APPLICANTON: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MMILHOO-1
CURRENT APPLICATION NUMBER: US/10/750,623
CURRENT APPLICATION NUMBER: US 60/437,482
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR APPLICATION VERSION 3.1
SEQ ID NOS: 64922
SOSTWARE: PARENT VERSION 3.1
LENGTH: 1685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              66 CTTCTACGCCTACTTGGGCGTCCTGCTGGTGGCCTGCTGCTCAACAGCCTGGCGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 36071, Application US/10750623
Publication No. US20050287531A1
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ORGANISM: Bovine 19866880675545
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US-10-750-623-36071
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RESULT 9

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APPLICANT: Merchiers, Pascal G.
APPLICANT: Hoffmann, Marcel
APPLICANT: Spittaels, Koenraad F. F.
APPLICANT: Spittaels, Koenraad F. F.
APPLICANT: Laenen, Wendy
TITLE OF INVENTION: Mendy
TITLE OF INVENTION: Amyloid-Beta Protein Production
FILE REFERENCE: P27,800-B USA
CURRENT FILING DATE: 2005-05-12
PRIOR PPLICATION NUMBER: 60/570,352
PRIOR PLING DATE: 2004-05-12
PRIOR PLING DATE: 2004-08-24
NUMBER OF SEQ ID NOS: 590
SOFTWARE: Patentin version 3.3
SEQ ID NO 5.29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1077;
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Pred. No. 4.3e-08;
0; Mismatches 308;
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Sequence 29, Application US/11127877 Publication No. US20050287565A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 49.3%;
Matches 311; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-127-877-29
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Gaps 9

Length 706;

110

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449 AGAGAGCAAGCTGCTTCTTGCTGTCTTCTACTGCATCCTGTTTGTATTTGGTCTTCTGGG 390
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              389 CAACAGCCTGGTCATCCTAGTCCTTGTCGCCTGCAAGAACTGAGGAGTGTCACGGATGT 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            269 CCACTATCAACTGGACCAGTGGGTATTCGGGACCGTAATGTGCAAGGTGGTCTCTGGCTT 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     329 ATACCTCTTGAACCTGGCCCTGTCTGACCTGCTTTTTGTCTTCTCCTTCCCCTTTCAGAC 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           231 GCACTCCCTGCGAGAC----ACCTCAGACACGCCGCTGTGCCAGCTCTCCCAGGGCAT 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        285 CTACCTGACCAACAGGTACATGAGCATCAGCCTGGTCACGGCCATCGCCGTGGACCGCTA 344
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51 AGCGATCAAGCTGGGCTTCTACGCCTACTTGGGCGTCCTGCTGGTGCTAGGCCTGCTGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              171 CTACATGACCAACCTGGCGGTGGCCGACCTCTGCCTGTGCGACCTTGCCCTTCGTGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 8.0%; Score 74.2; DB 7; Length 7
Best Local Similarity 51.1%; Pred. No. 3.8e-06;
Matches 203; Conservative 0; Mismatches 188; Indels
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; Publication No. US20050287531A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                ; TYPE: DNA
; ORGANISM: Bovine 19866880843412
US-10-750-185-32790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Bovine 19866880843412
                                                 SOFTWARE: PatentIN version 3.1
SEQ ID NO 32790
LENGTH: 706
NUMBER OF SEQ ID NOS: 64922
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US-10-750-623-32790/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   300 GTACATGAGCATCAGCCTGGTCACGGCCATCGCCGTGGACCGCTATGTGGCCGTGCGGGA 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           834 CTACTGCAGCATCCTCTTTCCTCACCTGCATCAGCGTGCACCGGTGCTGGGGGTCCTGCG 893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCCGCTGCGTGCCCGCGGGCTGCGGTCCCCCAGGCAGGCTGCGGCCGTGTGCGCGGTCCT 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           953
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                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Myoute, William M
TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
FILE REPERENCE: 031896-041000 (AM.01086)
CURRENT APPLICATION NUMBER: US/11/136,527
CURRENT FILING DATE: 2005-05-25
PRIOR PILING DATE: 2005-05-26
NUMBER OF SEQ ID NOS: 362830
SOFTWARE: Patentin version 3.2
SEQ ID NO 3805
LENGTH: 2011
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| Publication No. UB20050260603A1
| GENERAL INFORMATION:
| APPLICANT: PMI GENOMICS, INC.
| APPLICANT: PMI GENOMICS, INC.
| APPLICANT: ROSENFELD, David
| APPLICANT: ROSENFELD, David
| APPLICANT: ROSENFELD, David
| APPLICANT: BATES, Stephen
| APPLICANT: FANTIN, Dennis
| TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
| FILE REFERENCE: MMILION-2
| CURRENT APPLICATION NUMBER: US/10/750,185
| CURRENT PALING DATE: 203-12-31, CURRENT PALING DATE: 203-12-31, CURRENT PALING DATE: 203-12-31, CURRENT PALING DATE: 203-12-31, COURSENT PALING DATE: 203-12-31, COURSENT DA
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PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
                                                                                                                                                           ; Sequence 3805, Application US/11136527; Publication No. US20050287570A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Rattus norvegicus
US-11-136-527-3805
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Best Local Similarity 52.17
Matches 201, Conservative
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US-10-750-185-32790/c
                                                                                                                US-11-136-527-3805
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APPLICANT: MMI GENOMICS, INC.
APPLICANT: PAST S. Sue K.
APPLICANT: RESR, RICHARI
APPLICANT: ROSENFELD, David
APPLICANT: HOLM, Tom
APPLICANT: BATES, Stephen
APPLICANT: PANTIN, Dennis
TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MMILLOO-1
CURRENT APPLICATION NUMBER: US/10/750,623
FILE REPERING DATE: 2003-12-31
PRIOR PELLOR DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE PATENCIN VERSION 3.1
SEQ OFTWARE: PATENCIN VERSION 3.1
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Sequence 28, Application US/20050272054A1

GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: DETECTION AND USES THEREOF
TITLE OF INVENTION: DETECTION AND USES THEREOF
TITLE OF INVENTION: DOUGHER: US/10/995,561
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702

SOFTWARE: FASESEQ for Windows Version 4.0
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Best Local Similarity 51.0%; Pred. No. 9.4e-06;
Matches 203; Conservative 1; Mismatches 182; Indels
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; Publication No. US20050287570A1
; Publication No. US20050287570A1
; APPLICANT: Wyeth
; APPLICANT: Wyeth
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REPERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR PILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: Patentin version 3.2
; SEQ ID NOS: 362830
                                                                                                                                                CAACAGCCTGGCGCTCTGGGGGTGTTCTGCTGCCATGCAGCAGTGGACGGAGACCCGCAT 170
                              449 AGAGAGCAAGCTGCTTCTTGCTGTCTTCTACTGCATCCTGTTTGTATTTGGTCTTCTGGG 390
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Pred. No. 7.1e-06;
0; Mismatches 335; Indels 15;
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US-11-136-527-3310
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Sequence 13206, Application US/10995561

Publication No. US200502720541

GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
TITLE OF INVENTION: DETECTION AND USES THERROF
TITLE OF INVENTION: DETECTION AND USES THERROF
TITLE OF INVENTION: DATE: 2004-11-24
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13208
LENGTH: 13428
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78 CTTGGGCGTCCTGCTGCTAGGCCTGCTGCTCAACAGCCTGGCGCTCTGGGTGTTCTG 137
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COGANISM: Homo sapiens
US-10-995-561-13208
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US-10-995-561-13208
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